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OM protein - protein search, using sw model

Run on: January 5, 2006, 21:43:11 ; Search time 13 Seconds  
(without alignments)  
10.445 Million cell updates/sec

Title: US-09-894-550-3

Perfect score: 83

Sequence: 1 TKGGQDITDFQILENQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA\_New.\*
- 1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 5: /cgn2\_6/prodata/1/pubpaa/US03\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	65.1	269	6	Sequence 535, App
2	54	65.1	303	6	Sequence 534, App
3	53	63.9	271	6	Sequence 533, App
4	41	49.4	1538	6	Sequence 772, App
5	41	49.4	5335	6	Sequence 777, App
6	41	49.4	5406	6	Sequence 774, App
7	41	49.4	5454	6	Sequence 775, App
8	41	49.4	5935	6	Sequence 776, App
9	37.5	45.2	622	6	Sequence 239, App
10	37.5	45.2	635	6	Sequence 67, App
11	37.5	45.2	701	6	Sequence 65, App
12	37.5	45.2	885	6	Sequence 240, App
13	37.5	45.2	885	6	Sequence 241, App
14	37	44.6	182	6	Sequence 5278, App
15	37	44.6	401	6	Sequence 3, Appli
16	37	44.6	456	7	Sequence 15, Appl
17	37	44.6	863	7	Sequence 2, Appli
18	36	43.4	398	7	Sequence 7, Appli
19	36	43.4	473	7	Sequence 138, App
20	36	43.4	487	7	Sequence 281, App
21	36	43.4	5291	7	Sequence 79, Appl
22	35	42.2	275	7	Sequence 113-424-79
23	35	42.2	1009	6	Sequence 186, App
24	35	42.2	1099	6	Sequence 4556, App
25	35	42.2	1199	6	Sequence 1126, App

Sequence 94, Appl  
Sequence 234, App  
Sequence 98, Appl  
Sequence 6, Appli  
Sequence 1648, App  
Sequence 99, Appl  
Sequence 2, Appli  
Sequence 2356, App  
Sequence 292, App  
Sequence 15, Appl  
Sequence 14, Appl  
Sequence 114, App  
Sequence 13, Appl  
Sequence 1507, App  
Sequence 666, App  
Sequence 19, Appl  
Sequence 4, Appli  
Sequence 1, Appli  
Sequence 210, App  
Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-10-995-561-535  
; Sequence 535, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 535  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-535

Query Match 65.1%; Score 54; DB 6; Length 269;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10  
Db 253 TKGGQDITDF 262

RESULT 2  
US-10-995-561-534  
; Sequence 534, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 534  
; LENGTH: 303  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-534

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Query Match      65.1%; Score 54; DB 6; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
   |||||
Db 287 TKGGQDITDF 296

RESULT 3
US-10-995-561-533
; Sequence 533, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 533
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-533

Query Match      63.9%; Score 53; DB 6; Length 271;
Best Local Similarity 78.6%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGQDITDFQILENQ 16
   | |||||
Db 257 GPPSITDFQILENQ 270

RESULT 4
US-10-995-561-772
; Sequence 772, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 1538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-772

Query Match      49.4%; Score 41; DB 6; Length 1538;
Best Local Similarity 43.8%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TKGGQDITDFQILENQ 16
   : | | | : | | |
Db 1476 SRRGSASDPDLLETQ 1491

RESULT 5
US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match      49.4%; Score 41; DB 6; Length 5335;
Best Local Similarity 43.8%; Pred. No. 83;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TKGGQDITDFQILENQ 16
   : | | | : | | |
Db 5344 SRRGSASDPDLLETQ 5359

RESULT 6
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match      49.4%; Score 41; DB 6; Length 5406;
Best Local Similarity 43.8%; Pred. No. 83;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TKGGQDITDFQILENQ 16
   : | | | : | | |
Db 5344 SRRGSASDPDLLETQ 5359

RESULT 7
US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775
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Query Match      49.4%; Score 41; DB 6; Length 5464;
Best Local Similarity 43.8%; Pred. No. 84;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TKGGQDITDFQILENQ 16
DB 5402 SRRGSDASDFDLLETTQ 5417

RESULT 8
US-10-995-561-776
; Sequence 776, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 5935
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-776

Query Match      49.4%; Score 41; DB 6; Length 5935;
Best Local Similarity 43.8%; Pred. No. 92;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TKGGQDITDFQILENQ 16
DB 5873 SRRGSDASDFDLLETTQ 5888

RESULT 9
US-10-055-877-239
; Sequence 239, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby

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FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 239
LENGTH: 622
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-239

Query Match      45.2%; Score 37.5; DB 6; Length 622;
Best Local Similarity 41.2%; Pred. No. 30;
Matches 7; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 TKGGQDITDF-QILENQ 16
DB 295 TTSGEDVRDFAKVLKNK 311

RESULT 10
US-10-055-877-67
; Sequence 67, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li

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; APPLICANT: Caaman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-67

Query Match 45.2%; Score 37.5; DB 6; Length 635;
Best Local Similarity 41.2%; Pred. No. 31;
Matches 7; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 TKGGQDITDF-QILENQ 16
Db 295 TTSGEDVRDFAKVLKKNK 311

RESULT 11
US-10-055-877-65
; Sequence 65, Application US/10055877
; Publication No. US2005028241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Adam
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond

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; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-65

Query Match 45.2%; Score 37.5; DB 6; Length 701;
Best Local Similarity 41.2%; Pred. No. 34;
Matches 7; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 TKGGQDITDF-QILENQ 16
Db 361 TTSGEDVRDFAKVLKKNK 377

RESULT 12
US-10-055-877-240
; Sequence 240, Application US/10055877
; Publication No. US2005028241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard

```

APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,478  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/263,351  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/272,870  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/275,990  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/275,927  
PRIOR FILING DATE: 2001-03-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 512  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 240  
LENGTH: 885  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-055-877-240

Query Match 45.2%; Score 37.5; DB 6; Length 885;  
Best Local Similarity 41.2%; Pred. No. 45;  
Matches 7; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 TKGQDITDF-QILENQ 16  
Db 563 TTSGEDVRDFAKVLKKNK 579

RESULT 13  
US-10-055-877-241  
Sequence 241, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: DeCristofaro, Marc  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchernev, Velizar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spytak, Kimberly  
APPLICANT: Ratelli, Luca  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Eisen, Andrew

APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shimkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,478  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/263,351  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/272,870  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/275,990  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/275,927  
PRIOR FILING DATE: 2001-03-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 512  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 241  
LENGTH: 885  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-055-877-241

Query Match 45.2%; Score 37.5; DB 6; Length 885;  
Best Local Similarity 41.2%; Pred. No. 45;  
Matches 7; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 TKGQDITDF-QILENQ 16  
Db 563 TTSGEDVRDFAKVLKKNK 579

RESULT 14  
US-10-467-657-5278  
Sequence 5278, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON Spa  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 5278  
LENGTH: 182

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; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5276

Query Match      44.6%; Score 37; DB 6; Length 182;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QDITDFQILE 14
Db      104 QDLSDYQVVE 113

RESULT 15
US-11-097-749-3
; Sequence 3, Application US/11097749
; Publication No. US20050267028A1
; GENERAL INFORMATION:
; APPLICANT: VIRJI, MUMTAZ
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES
; FILE REFERENCE: 63221(50221)
; CURRENT APPLICATION NUMBER: US/11/097,749
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: GB0419594.7
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: GB0408390.3
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: GB2003/004273
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: GB0222764.3
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-097-749-3

Query Match      44.6%; Score 37; DB 7; Length 401;
Best Local Similarity 63.6%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      6 DITDFOILENQ 16
Db      232 DVQDKQILQNG 242

Search completed: January 5, 2006, 21:51:44
Job time : 13 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 5, 2006, 21:35:50 ; Search time 235 Seconds

(without alignments)  
48.036 Million cell updates/sec

Title: US-09-894-550-3

Perfect score: 83

Sequence: 1 TKGGQDITDFQILENQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	67.5	271	1 IL1A CERTO	P46647 cercocebub
2	56	67.5	271	1 IL1A MACFA	P79340 macaca fasc
3	56	67.5	271	1 IL1A MACMU	P48089 macaca mula
4	56	67.5	271	2 Q4R4F0 MACFA	Q4R4F0 macaca fasc
5	55.5	66.9	267	1 IL1B FELCA	P41687 felis silve
6	54	65.1	153	2 Q43645 HUMAN	Q43645 homo sapien
7	54	65.1	193	2 Q8HXR5_PANTR	Q8HXR5 pan troglod
8	54	65.1	269	1 IL1B HUMAN	P01584 homo sapien
9	54	65.1	269	2 Q53X59 HUMAN	Q53X59 homo sapien
10	54	65.1	269	2 Q53XX2 HUMAN	Q53XX2 homo sapien
11	54	65.1	269	2 Q8MKH3_SAIISC	Q8MKH3 salmiri sci
12	54	65.1	270	1 IL1B EUMTU	Q6r2x3 eumetopias
13	54	65.1	270	2 Q6PUD2_PHOVI	Q6pud2 phoca vitul
14	53	63.9	271	1 IL1A HUMAN	P01583 homo sapien
15	53	63.9	271	2 Q53QF9 HUMAN	Q53QF9 homo sapien
16	52	62.7	270	1 IL1A HORSE	Q28385 equus cabal
17	51	61.4	152	2 Q8HXR6 MACFA	Q8HXR6 macaca fasc
18	51	61.4	268	1 IL1B MACFA	P79182 macaca fasc
19	51	61.4	269	1 IL1B CERTO	P46648 cercocebub
20	51	61.4	269	1 IL1B MACMU	P48090 macaca mula
21	51	61.4	269	1 IL1B MACNE	P51493 macaca neme
22	50	60.2	270	1 IL1A PIG	P18430 sus scrofa
23	48	57.8	113	2 Q5MAC0 BOVIN	Q5mac0 bos taurus
24	48	57.8	266	1 IL1B CAPHI	P79162 capra hircu
25	48	57.8	286	1 IL1B CEREL	P51745 cervus elap
26	48	57.8	266	1 IL1B SHEEP	P21621 ovis aries
27	48	57.8	266	2 Q6R498 BUBBU	Q6r498 bubalus bub
28	48	57.8	266	2 Q6R750_9CETA	Q6r750 odocoileus
29	48	57.8	581	2 Q8KVT7_STRCO	Q8kvt7 streptomyc
30	48	57.8	802	2 Q9KXMS_STRCO	Q9kxms streptomyc
31	47.5	57.2	268	1 IL1B HORSE	Q28386 equus cabal

32	47	56.6	267	1 IL1B LAMGL	Q865x8 lama glama
33	46	55.4	270	1 IL1A FELCA	Q46613 felis silve
34	46	55.4	344	2 Q5FTK8_GLUOX	Q5ftk8 gluconobact
35	46	55.4	888	2 Q9VAE9_DROME	Q9vae9 drosophila
36	45	54.2	266	2 Q8WNR2_DELE	Q8wnr2 delphinapte
37	45	54.2	266	2 Q9TTK1_TURTR	Q9ttk1 tursiops tr
38	45	54.2	879	2 Q4RNB6_TETNG	Q4rnb6 tetracodon n
39	45	54.2	908	2 Q90ZQ1_OREMO	Q90zq1 oreochromis
40	45	54.2	908	2 Q90ZQ2_OREMO	Q90zq2 oreochromis
41	45	54.2	919	2 Q90ZQ3_OREMO	Q90zq3 oreochromis
42	45	54.2	919	2 Q90ZQ4_OREMO	Q90zq4 oreochromis
43	45	54.2	930	2 Q8UUK3_OREMO	Q8uuk3 oreochromis
44	45	54.2	930	2 Q8UUK4_OREMO	Q8uuk4 oreochromis
45	45	54.2	963	2 Q91084_MORCS	Q91084 morone chry

## ALIGNMENTS

### RESULT 1

IL1A CERTO  
ID IL1A CERTO STANDARD; PRT; 271 AA.

AC P46647;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Interleukin-1 alpha precursor (IL-1 alpha).

GN Name=IL1A;

OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopitheidae; Cercopithecinæ; Cercocebus.

OX NCBI\_TaxID=9531;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Blood;

RX MEDLINE=96003435; PubMed=75611102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and

nonhuman primates.";

RT J. Immunol. 155:3946-3954(1995).

RL FUNCTION: Produced by activated macrophages, IL-1 stimulates

thymocyte proliferation by inducing IL-2 release, B-cell

maturation and proliferation, and fibroblast growth factor

activity. IL-1 proteins are involved in the inflammatory response,

being identified as endogenous pyrogens, and are reported to

stimulate the release of prostaglandin and collagenase from

synovial cells.

CC SUBUNIT: Monomer.

CC SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic

segment in the precursor sequence suggests that IL-1 is released

by damaged cells or is secreted by a mechanism differing from that

used for other secretory proteins.

CC DOMAIN: The similarity among the IL-1 precursors suggests that the

amino ends of these proteins serve some as yet undefined function.

CC SIMILARITY: Belongs to the IL-1 family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use as long as its content is in no way modified and this statement is not

removed.

DR EMBL; U19836; AAA86703.1; -; mRNA.

DR HSSP; P01583; IITA.

DR InterPro; IPR003502; IL1\_propep.

DR InterPro; IPR000975; Interleukin1.

DR InterPro; IPR003295; InterleukinIL1A.

DR InterPro; IPR003294; InterleukinIL1AB.

DR PANTHER; PTHR11420; InterleukinIL1A; 1.

DR Pfam; PF00340; IL1; 1.

DR Pfam; PF02394; IL1\_propep; 1.

DR PRINTS; PR00264; INTERLEUKIN1.

```
DR PRINTS; PR01358; INTRLEUKIN1A.
DR PRINTS; PR01357; INTRLEUKIN1AB.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SMO0125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Glycoprotein; Inflammatory response; Macrophage; Mitogen;
KW Pyrogen.
FT PROPEP 1 112 By similarity.
FT CHAIN 113 271 Interleukin-1 alpha.
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 271 AA; 30451 MW; 19BDFB29A5D51A58 CRC64;

Query Match 67.5%; Score 56; DB 1; Length 271;
Best Local Similarity 80.0%; Pred. No. 0.47;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KGGQDITDFQILENQ 16
|||
DB 256 KGLPSITDFQILENQ 270

RESULT 2
IL1A_MACFA
ID IL1A_MACFA STANDARD; PRT; 271 AA.
AC P79340;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1).
GN Name=IL1A;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates
CC thymocyte proliferation by inducing IL-2 release, B-cell
CC maturation and proliferation, and fibroblast growth factor
CC activity. IL-1 proteins are involved in the inflammatory response,
CC being identified as endogenous pyrogens, and are reported to
CC stimulate the release of prostaglandin and collagenase from
CC synovial cells (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic
CC segment in the precursor sequence suggests that IL-1 is released
CC by damaged cells or is secreted by a mechanism differing from that
CC used for other secretory proteins.
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the
CC amino ends of these proteins serve some as yet undefined function.
CC -!- SIMILARITY: Belongs to the IL-1 family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; AB000553; BAA19147.1; -; mRNA.
DR HSSP; P01583; IITA.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003295; InterleukinIL1A.
DR InterPro; IPR003294; InterleukinIL1AB.
DR PANTHER; PTHR11420; InterleukinIL1A; 1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01358; INTRLEUKIN1A.
```

```
DR PRINTS; PR01357; INTRLEUKIN1AB.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SMO0125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Glycoprotein; Inflammatory response; Macrophage; Mitogen;
KW Pyrogen.
FT PROPEP 1 112 By similarity.
FT CHAIN 113 271 Interleukin-1 alpha.
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 271 AA; 30686 MW; 0526A9A6404558F0 CRC64;

Query Match 67.5%; Score 56; DB 1; Length 271;
Best Local Similarity 80.0%; Pred. No. 0.47;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KGGQDITDFQILENQ 16
|||
DB 256 KGLPSITDFQILENQ 270

RESULT 3
IL1A_MACMU
ID IL1A_MACMU STANDARD; PRT; 271 AA.
AC P48089;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1).
GN Name=IL1A;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates
CC thymocyte proliferation by inducing IL-2 release, B-cell
CC maturation and proliferation, and fibroblast growth factor
CC activity. IL-1 proteins are involved in the inflammatory response,
CC being identified as endogenous pyrogens, and are reported to
CC stimulate the release of prostaglandin and collagenase from
CC synovial cells.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic
CC segment in the precursor sequence suggests that IL-1 is released
CC by damaged cells or is secreted by a mechanism differing from that
CC used for other secretory proteins.
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the
CC amino ends of these proteins serve some as yet undefined function.
CC -!- SIMILARITY: Belongs to the IL-1 family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; U19844; AAA86708.1; -; mRNA.
DR HSSP; P01583; IITA.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003295; InterleukinIL1A.
DR InterPro; IPR003294; InterleukinIL1AB.
```



DR PANTHER: PTHR11420; InterleukinIL1A; 1.  
 DR Pfam; PF00340; IL1; 1.  
 DR PRINTS; PR00264; IL1\_propep; 1.  
 DR PRINTS; PR01358; INTERLEUKIN1.  
 DR PRINTS; PR01357; INTRLEUKIN1A.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 DR Cytokine; Glycoprotein; Inflammatory response; Macrophage; Mitogen;  
 KW Pyrogen.  
 FT CHAIN 1 112 By similarity.  
 FT CARBOHYD 102 121 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 271 AA; 30693 MW; 1DB6BC7C5E5B438E CRC64;  
 Query Match 67.5%; Score 56; DB 1; Length 271;  
 Best Local Similarity 80.0%; Pred. No. 0.47;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 KGGQDITDFQILENQ 16  
 DB 256 KGLPSITDFQILENQ 270  
 RESULT 4  
 Q4R4F0\_MACFA  
 ID Q4R4F0 MACFA PRELIMINARY; PRT; 271 AA.  
 AC Q4R4F0;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Testis cDNA clone: QtsA-10268, similar to human interleukin 1, alpha (IL1A).  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA International consortium for macaque cDNA sequencing, analysis;  
 RT "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications."  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gotohori T., Shen J.C.-K., Wu C.I., Hashimoto K.;  
 RT "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB178964; BA00151; -; mRNA.  
 DR InterPro; IPR003502; IL1\_propep.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR InterPro; IPR003295; InterleukinIL1A.  
 DR InterPro; IPR003294; InterleukinIL1AB.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR PRINTS; PR01358; INTERLEUKIN1A.  
 DR PRINTS; PR01357; INTRLEUKIN1A.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Inflammatory response; Mitogen; Pyrogen.  
 FT CHAIN 271 AA; 30718 MW; 4FE8959FCE79B00B CRC64;  
 SQ SEQUENCE 271 AA; 30718 MW; 4FE8959FCE79B00B CRC64;  
 Query Match 67.5%; Score 56; DB 2; Length 271;

Best Local Similarity 80.0%; Pred. No. 0.47;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 KGGQDITDFQILENQ 16  
 DB 256 KGLPSITDFQILENQ 270  
 RESULT 5  
 IL1B\_FELCA  
 ID IL1B\_FELCA STANDARD; PRT; 267 AA.  
 AC P41687;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Interleukin-1 beta precursor (IL-1 beta).  
 GN Name=il1b;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
 OC Felinae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Bone marrow;  
 RA Daniel S.L., Brenner C.A., Legendre A.M., Soloman A., Rouse B.T.;  
 RT "Feline cytokines TNF alpha and IL-1 beta: PCR cloning and sequencing of cDNA."  
 RL Anim. Biotechnol. 3:117-121(1992).  
 CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates thymocyte proliferation by inducing IL-2 release, B-cell maturation and proliferation, and fibroblast growth factor activity. IL-1 proteins are involved in the inflammatory response, being identified as endogenous pyrogens, and are reported to stimulate the release of prostaglandin and collagenase from synovial cells.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic segment in the precursor sequence suggests that IL-1 is released by damaged cells or is secreted by a mechanism differing from that used for other secretory proteins.  
 CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the amino ends of these proteins serve some as yet undefined function.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC EMBL; M92060; AAA30814.1; -; mRNA.  
 DR HSSP; P01584; 1HTB.  
 DR SMR; P41687; 116-267.  
 DR InterPro; IPR002348; IL1\_HBGF.  
 DR InterPro; IPR003502; IL1\_propep.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR InterPro; IPR003294; InterleukinIL1AB.  
 DR InterPro; IPR003296; InterleukinIL1B.  
 DR PANTHER; PTHR10078; SFI; InterleukinIL1B; 1.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR PRINTS; PR01359; INTRLEUKIN1B.  
 DR PRINTS; PR01357; INTRLEUKIN1A.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Cytokine; Inflammatory response; Macrophage; Mitogen; Pyrogen.  
 FT CHAIN 1 115 By similarity.  
 FT PROPEP 115 267 Interleukin-1 beta.  
 FT CHAIN 116 267 Interleukin-1 beta.  
 SQ SEQUENCE 267 AA; 30362 MW; 781P9971E32F6AE1 CRC64;

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Query Match      66.9%; Score 55.5; DB 1; Length 267;
Best Local Similarity 80.0%; Pred. No. 0.56;
Matches 12; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Oy 1 TKGQDITDFQILEN 15
    |||||
Db 252 TKGQDITDF-IMES 265

RESULT 6
O43645 HUMAN
ID O43645 HUMAN PRELIMINARY; PRT; 153 AA.
AC O43645
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 1 beta (Fragment).
GN Name=IL1b;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043335; AAC03536.1; -; mRNA.
DR HSSP; P01584; 1H1B.
DR SMR; O43645; 1-153.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003294; InterleukinIL1B.
DR InterPro; IPR003296; InterleukinIL1A.
DR InterPro; IPR003297; InterleukinIL1RA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.
DR PRINTS; PR01360; INTRLEUKIN1X.
DR PRINTS; PR01357; INTRLEUKIN1A.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR NON TER 1
FT SEQUENCE 153 AA; 17426 MW; A1AB2B5FE8B47146 CRC64;

Query Match      65.1%; Score 54; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TKGQDITDF 10
    |||||
Db 137 TKGQDITDF 146

RESULT 7
Q8HXR5 PANTR
ID Q8HXR5 PANTR PRELIMINARY; PRT; 193 AA.
AC Q8HXR5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-1 beta (Fragment).
GN Name=IL1B;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.

Query Match      65.1%; Score 54; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TKGQDITDF 10
    |||||
Db 137 TKGQDITDF 146

RESULT 8
IL1B_HUMAN
ID IL1B_HUMAN STANDARD; PRT; 269 AA.
AC P01584; Q7RU01; Q9GHES; Q9UCT6;
DT 21-JUL-1986 (Rel. 01, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta) (Catabolin).
GN Name=IL1B; Synonyms=IL1F2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=85088517; PubMed=6083565;
RA Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Dinarello C.A.;
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=85240547; PubMed=2989698;
RA March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA Hopp T.P., Cosman D.;
RT "Cloning, sequence and expression of two distinct human interleukin-1
complementary DNAs.";
RL Nature 315:641-647(1985).
RN [3]
```

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OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22344682; PubMed=12356774; DOI=10.1074/jbc.M206636200;
RA Smith D.E., Ketchum R.R., Moore H., Anderson Z., Renshaw B.R.,
RA Friend D.J., Sims J.E.;
RT "A single amino acid difference between human and monkey interleukin
(IL)-1beta dictates effective binding to soluble type II IL-1
receptor.";
RL J. Biol. Chem. 277:47619-47625(2002).
DR EMBL; AY172104; AAN76443.1; -; mRNA.
DR HSSP; P01584; 211B.
DR SMR; Q8HXR5; 41-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0001660; P:fever; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003294; InterleukinIL1A.
DR InterPro; IPR003296; InterleukinIL1B.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.
DR PRINTS; PR01357; INTRLEUKIN1A.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR NON TER 1
FT SEQUENCE 193 AA; 22233 MW; 8C45E22FC3D7FD37 CRC64;

Query Match      65.1%; Score 54; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TKGQDITDF 10
    |||||
Db 177 TKGQDITDF 186
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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=87040762; PubMed=3490554;  
RA Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;  
RT "Genomic sequence for human prointerleukin 1 beta: possible evolution  
from a reverse transcribed prointerleukin 1 alpha gene.";  
RL Nucleic Acids Res. 14:7897-7914(1986).  
RN [4]  
RP ERRATUM.  
RA Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;  
RL Nucleic Acids Res. 15:868-868(1987).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=87248099; PubMed=2954882; DOI=10.1016/0378-1119(87)90398-2;  
RA Bensi G., Raugi G., Palla E., Carinci V., Buonamassa D.T., Melli M.;  
RT "Human interleukin-1 beta gene.";  
RL Gene 52:95-101(1987).  
RN [6]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=87156769; PubMed=3493774;  
RA Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,  
RA Nakai S., Hirai Y.;  
RT "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell  
line.";  
RL Biochem. Biophys. Res. Commun. 143:345-352(1987).  
RN [7]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=90249285; PubMed=2635664;  
RA Korenko S.V., Bulecnik M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,  
RA Emel'yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,  
RA Kurbatova T.V., Reshetnikov V.B., Simbirtsev A.S., Kelinskii S.A.,  
RA Vinetskii Y.P.;  
RT "Cloning of the cDNA coding for human prointerleukin-1 alpha and  
prointerleukin-1 beta.";  
RL Dokl. Akad. Nauk SSSR 309:1005-1008(1989).  
RN [8]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;  
RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,  
RA Korman K.;  
RT "A sequence-based map of the nine genes of the human interleukin-1  
cluster.";  
RL Genomics 79:718-725(2002).  
RN [9]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
RA Rajkumar N.R., Toch E.J., Yi Q., Nickerson D.A.;  
RT "SeattleSNPs. NHLBI HL6682 program for genomic applications, UW-  
PHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uddin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shervchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [11]  
RP PROTEIN SEQUENCE OF 117-128.  
RX MEDLINE=88184226; PubMed=3281727;  
RA Zeebo K.M., Wypych J., Yuschenkoff V.N., Lu H., Hunt P., Dukes P.P.,  
RA Langley K.E.;  
RT "Effects of hematopoietin-1 and interleukin 1 activities on early  
hematopoietic cells of the bone marrow.";  
RL Blood 71:962-968(1988).  
RN [12]  
RP PROTEIN SEQUENCE OF 114-135.  
RC TISSUE=Skin;  
RX MEDLINE=92013781; PubMed=1919436; DOI=10.1084/jem.174.4.821;  
RA Mizutani H., Schecter N., Lazarus G., Black R.A., Kupper T.S.;  
RT "Rapid and specific conversion of precursor interleukin 1 beta (IL-1  
beta) to an active IL-1 species by human mast cell chymase.";  
RL J. Exp. Med. 174:821-825(1991).  
RN [13]  
RP RECEPTOR BINDING.  
RX MEDLINE=92110334; PubMed=1837236; DOI=10.1016/0167-4838(91)90437-5;  
RA Nanduri V.B., Hulmes J.D., Pan Y.C., Kilian P.L., Stern A.S.;  
RT "The role of arginine residues in interleukin 1 receptor binding.";  
RL Biochim. Biophys. Acta 1118:25-35(1991).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RX MEDLINE=88211543; PubMed=3259176;  
RA Priestle J.P., Schar H.-P., Grutter M.G.;  
RT "Crystal structure of the cytokine interleukin-1 beta.";  
RL EMBO J. 7:339-343(1988).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=90093925; PubMed=2602367;  
RA Priestle J.P., Schar H.-P., Gruetter M.G.;  
RT "Crystallographic refinement of interleukin 1 beta at 2.0-A  
resolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=90064532; PubMed=2585509;  
RA Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,  
RA Watenpaugh K.D., Einspahr H.M.;  
RT "Crystal structure of recombinant human interleukin-1 beta at 2.0-A  
resolution.";  
RL J. Mol. Biol. 209:779-791(1989).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.  
RX MEDLINE=97215903; PubMed=9062193;  
RA Vigers G.P.A., Anderson L.J., Caffes P., Brandhuber B.J.;  
RT "Crystal structure of the type-I interleukin-1 receptor complexed with  
interleukin-1beta.";  
RL Nature 386:190-194(1997).  
RN [18]  
RP STRUCTURE BY NMR.  
RX MEDLINE=90321925; PubMed=2372550;  
RA Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;  
RT "Determination of the secondary structure and molecular topology of  
interleukin-1 beta by use of two- and three-dimensional heteronuclear  
15N-1H NMR spectroscopy.";  
RL Biochemistry 29:4668-4682(1990).  
RN [19]  
RP STRUCTURE BY NMR.  
RX MEDLINE=91159409; PubMed=2001363;  
RA Clore G.M., Wingfield P.T., Gronenborn A.M.;  
RT "High-resolution three-dimensional structure of interleukin 1 beta in  
solution by three- and four-dimensional nuclear magnetic resonance  
spectroscopy.";  
RL Biochemistry 30:2315-2323(1991).  
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates  
thymocyte proliferation by inducing IL-2 release, B-cell  
maturation and proliferation, and fibroblast growth factor  
activity. IL-1 proteins are involved in the inflammatory response,  
being identified as endogenous pyrogens, and are reported to  
stimulate the release of prostaglandin and collagenase from  
synovial cells.

CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic  
 CC segment in the precursor sequence suggests that IL-1 is released  
 CC by damaged cells or is secreted by a mechanism differing from that  
 CC used for other secretory proteins.  
 CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the  
 CC amino ends of these proteins serve some as yet undefined function.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; K02770; AAA36106.1; -; mRNA.  
 DR EMBL; M54933; AAA59136.1; ALT SEQ; mRNA.  
 DR EMBL; K02532; CAA26372.1; -; mRNA.  
 DR EMBL; X04500; CAA28185.1; -; Genomic DNA.  
 DR EMBL; M15840; AAA74137.1; -; Genomic DNA.  
 DR EMBL; M15330; AAA59135.1; -; mRNA.  
 DR EMBL; X56087; CAA39567.1; -; mRNA.  
 DR EMBL; BN000002; CAD29872.1; -; Genomic DNA.  
 DR EMBL; AY137079; AAM88883.1; -; Genomic DNA.  
 DR EMBL; BC008678; AAO8678.1; -; mRNA.

Query Match 65.1%; Score 54; DB 1; Length 269;

Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10

Db 253 TKGGQDITDF 262

# RESULT 9

Q53X59\_HUMAN  
 ID Q53X59\_HUMAN PRELIMINARY; PRT; 269 AA.  
 AC Q53X59;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT IL1B protein (Fragment).  
 DE Name=IL1B;  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
 RT "Cloning of human full open reading frames in Gateway(TM) system entry  
 RT vector (pDONR201).";  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR407679; CAG28607.1; -; mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006954; P:inflammatory response; IEA.  
 KW Inflammatory response; Mitogen; Pyrogen.  
 FT NON TER 269  
 SQ SEQUENCE 269 AA; 30747 MW; AD193C31C566FD64 CRC64;

Query Match 65.1%; Score 54; DB 2; Length 269;

Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10

Db 253 TKGGQDITDF 262

# RESULT 10

Q53XX2\_HUMAN PRELIMINARY; PRT; 269 AA.

Q53XX2\_HUMAN PRELIMINARY; PRT; 269 AA.  
 AC Q53XX2;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DT Interleukin 1, beta (Hypothetical protein IL1B).  
 DE Name=IL1B;  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,  
 RA Phelan M., Farmer A.;  
 RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor  
 RT vector.";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cotton M., Andrews S., Doebber A., Rose C.;  
 RA "The sequence of Homo sapiens BAC clone RP11-67L14.";  
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Waterston R.H.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Waterston R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wilson R.K.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT007213; AAF35877.1; -; mRNA.  
 DR EMBL; AC079753; AAX88888.1; -; Genomic DNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006954; P:inflammatory response; IEA.  
 KW Hypothetical protein; Inflammatory response; Mitogen; Pyrogen.  
 SQ SEQUENCE 269 AA; 30748 MW; 9BF73C673C6FD66 CRC64;

Query Match 65.1%; Score 54; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10  
 Db 253 TKGGQDITDF 262

RESULT 11  
 Q8MKH3\_SAISC  
 ID Q8MKH3\_SAISC PRELIMINARY; PRT; 269 AA.  
 AC Q8MKH3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Interleukin-1 beta.  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;  
 OC Cebinae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINS=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;  
 RA Heraud J.M., Lavergne A., Kazanji M.;  
 RT "Molecular cloning, characterization, and quantification of squirrel

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PT monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL Immunogenetics 54:20-29(2002).
DR EMBL; AF294754; AAK92041.1; -, mRNA.
DR HSBP; P01584; IL2H.
DR SMR; Q8MKH3; 117-269.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0001660; P:fever; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR003294; InterleukinIL1AB.
DR InterPro; IPR003296; InterleukinIL1B.
DR InterPro; IPR003297; InterleukinIL1RA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.
DR PRINTS; PR01357; INTRLEUKIN1A.
DR PRINTS; PR01360; INTRLEUKIN1AB.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Inflammatory response; Mitogen; Pyrogen.
FT CHAIN 119 270 Interleukin-1 beta.
SQ SEQUENCE 269 AA; 30800 MW; 50FAC2B21501B1F2 CRC64;

Query Match 65.1%; Score 54; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10
DB 253 TKGGQDITDF 262

RESULT 12
IL1B_EUMJU STANDARD; PRT; 270 AA.
AC Q6R2X3;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN Name=IL1B;
OS Eumetopias jubatus (Steller sea lion).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Pinnipedia; Otariidae;
OC Eumetopias.
OC NCBI_TaxID=34886;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bozza M., Atkinson S.;
RT "Molecular cloning of Steller sea lion (Eumetopias jubatus) interleukin-1 beta (IL-1beta) from a LPS-stimulated mononuclear cell cDNA library.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Produced by activated macrophages, IL-1 stimulates thymocyte proliferation by inducing IL-2 release, B-cell maturation and proliferation, and fibroblast growth factor activity. IL-1 proteins are involved in the inflammatory response, being identified as endogenous pyrogens, and are reported to stimulate the release of prostaglandin and collagenase from synovial cells (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic segment in the precursor sequence suggests that IL-1 is released by damaged cells or is secreted by a mechanism differing from that used for other secretory proteins.
CC -1- DOMAIN: The similarity among the IL-1 precursors suggests that the amino ends of these proteins serve some as yet undefined function.

CC -1- SIMILARITY: Belongs to the IL-1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; AY517546; AAR98779.1; -, mRNA.
DR SMR; O6R2X3; 119-270.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003294; InterleukinIL1AB.
DR InterPro; IPR003296; InterleukinIL1B.
DR PANTHER; PTHR10078:SF1; InterleukinIL1B; 1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.
DR PRINTS; PR01357; INTRLEUKIN1A.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Inflammatory response; Macrophage; Mitogen; Pyrogen.
FT PROPEP 1 118 By similarity.
FT CHAIN 119 270 Interleukin-1 beta.
SQ SEQUENCE 270 AA; 30887 MW; F48CDB5EC29981C CRC64;

Query Match 65.1%; Score 54; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10
DB 255 TKGGQDITDF 264

RESULT 13
Q6PUD2_PHOVI PRELIMINARY; PRT; 270 AA.
AC Q6PUD2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-1 beta.
OS Phoca vitulina richardsi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Pinnipedia; Phocidae;
OC Phoca.
OC NCBI_TaxID=271025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bozza M., Atkinson S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY578791; AAS91558.1; -, mRNA.
DR SMR; Q6PUD2; 119-270.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0001660; P:fever; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR003294; InterleukinIL1AB.
DR InterPro; IPR003296; InterleukinIL1B.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.

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DR PRINTS; PR01357; INTRLEUKNIAB.
DR PRODom; PD002536; Interleukin_1; 1.
DR SMART; SMO0125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Inflammatory response; Mitogen; Pyrogen.
SQ SEQUENCE 270 AA; 31052 MW; 36972890C6A2FB2E CRC64;

Query Match 65.1%; Score 54; DB 2; Length 270;
Best Local Similarity 100.0%; Pred.No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10
   |||||
DB 255 TKGGQDITDF 264

RESULT 14
IL1A_HUMAN
ID IL1A_HUMAN STANDARD; PRT; 271 AA.
AC P01583; Q7RU02;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1).
GN Name=IL1A; Synonyms=IL1F1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=85240547; PubMed=2989698;
RA March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA Hopp T.P., Cosman D.;
RT "Cloning, sequence and expression of two distinct human interleukin-1
RT complementary DNAs.";
RL Nature 315:641-647(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86205226; PubMed=3486405;
RA Furutani Y., Notake M., Fukui T., Ohue M., Nomura H., Yamada M.,
RA Nakamura S.;
RT "Complete nucleotide sequence of the gene for human interleukin 1
RT alpha.";
RL Nucleic Acids Res. 14:3167-3179(1986).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT SER-114.
RX MEDLINE=85297782; PubMed=2994016;
RA Furutani Y., Notake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
RT "Cloning and characterization of the cDNAs for human and rabbit
RT interleukin-1 precursor.";
RL Nucleic Acids Res. 13:5869-5882(1985).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT SER-114.
RX MEDLINE=90249285; PubMed=2635664;
RA Korenko S.V., Buleikov M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,
RA Emel'yanov A.V., Kotlov A.P., Konusova V.G., Kotov A.Y.,
RA Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,
RA Vinetskii Y.P.;
RT "Cloning of the cDNA coding for human prointerleukin-1 alpha and
RT prointerleukin-1 beta.";
RL Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86141855; PubMed=3485152;
RA Gubler U., Chua A.O., Stern A.S., Hellmann C.P., Vitek M.P.,
RA Dechiara T.M., Benjamin W.R., Collier K.J., Dukovich M.,
RA Fanilietti P.C., Fiedler-Nagy C., Jensen J., Kaffka K., Kilian P.L.,
RA Stremlo D., Wittreich B.H., Woehle D., Mizel S.B., Lomedico P.T.;
RT "Recombinant human interleukin 1 alpha: purification and biological

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RT RT
RL J. Immunol. 136:2492-2497(1986).
RN [6]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=87156769; PubMed=3493774;
RA Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
RA Nakai S., Hirai Y.;
RT "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
RT line.";
RL Biochem. Biophys. Res. Commun. 143:345-352(1987).
RN [7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
RA Kornman K.;
RT "A sequence-based map of the nine genes of the human interleukin-1
RT cluster.";
RL Genomics 79:718-725(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLN-85; SER-114 AND
RN ASN-138.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattlesNPs. NHLBI HL6682 program for genomic applications, UW-
RT FHCRS, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schemm A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP PROTEIN SEQUENCE OF IL13-132.
RX MEDLINE=88184226; PubMed=3281727;
RA Zsebo K.M., Wypych J., Yushchenko V.N., Lu H., Hunt P., Dukes P.P.,
RA Langley K.E.;
RT "Effects of hematopoietin-1 and interleukin 1 activities on early
RT hematopoietic cells of the bone marrow.";
RL Blood 71:962-968(1988).
RN [13]

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RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
RX MEDLINE=90268016; PubMed=2346741;  
RA Graves B.J., Hatada M.H., Hendrickson W.A., Miller J.K., Madison V.S.,  
RA Satow Y.;  
RT "Structure of interleukin 1 alpha at 2.7-A resolution.";  
RL Biochemistry 29:2679-2684(1990).  
RN [14]  
RP MYRISTOYLATION.  
RX MEDLINE=93348250; PubMed=8346241;  
RA Stevenson F.T., Bursten S.L., Fanton C., Locksley R.M., Lovett D.H.;  
RT "The 31-kDa precursor of interleukin 1 alpha is myristoylated on  
RT specific lysines within the 16-kDa N-terminal piece.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:7245-7249(1993).  
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates  
CC thymocyte proliferation by inducing IL-2 release, B-cell  
CC maturation and proliferation, and fibroblast growth factor  
CC activity. IL-1 proteins are involved in the inflammatory response,  
CC being identified as endogenous pyrogens, and are reported to  
CC stimulate the release of prostaglandin and collagenase from  
CC synovial cells.  
CC  
CC -!- SUBUNIT: Monomer.  
CC  
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic  
CC segment in the precursor sequence suggests that IL-1 is released  
CC by damaged cells or is secreted by a mechanism differing from that  
CC used for other secretory proteins.  
CC  
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the  
CC amino ends of these proteins serve some as yet undefined function.  
CC  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC -----  
DR EMBL; X02531; CAA26371.1; -; mRNA.  
DR EMBL; X03833; CAA27448.1; -; Genomic\_DNA.  
DR EMBL; X02851; CAA26604.1; -; mRNA.  
DR EMBL; X56086; CAA39566.1; -; mRNA.  
DR EMBL; M28983; AAS59134.1; -; mRNA.  
DR EMBL; M15329; AAS59133.1; -; mRNA.  
DR EMBL; BN000002; CAD29871.1; -; Genomic\_DNA.  
DR EMBL; BF007014; RAP35660.1; -; mRNA.  
DR EMBL; CA457414; CAG33695.1; -; mRNA.  
DR EMBL; AF536338; AAM96189.1; -; Genomic\_DNA.  
DR EMBL; BC013142; AAH13142.1; -; mRNA.  
DR PIR; A23385; ICHUIA.  
DR PDB; 1ITA; Model; @=121-271.  
DR PDB; 2ILA; X-ray; @=117-271.  
DR Ensembl; ENSG00000115008; Homo sapiens.  
DR HGNC; HGNC:5991; IL1A.  
DR H-InvDB; HIX0002385; -.  
DR MIM; 147760; -.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0003125; F:cytokine activity; TAS.  
DR GO; GO:0004871; F:signal transducer activity; TAS.  
DR GO; GO:0006916; P:anti-apoptosis; TAS.  
DR GO; GO:0006915; P:apoptosis; TAS.  
DR GO; GO:0008283; P:cell proliferation; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
DR InterPro; IPR003502; IL1\_propep.  
DR InterPro; IPR000975; Interleukin\_1.  
DR InterPro; IPR003295; Interleukin\_IL1A.  
DR InterPro; IPR003294; Interleukin\_IL1AB.  
DR PANTHER; PTHR11420; InterleukinIL1A, 1.  
DR Pfam; PF00340; IL1; 1.  
DR Pfam; PF02394; IL1\_propep; 1.  
DR PRINTS; PR00264; INTERLEUKIN1.  
DR PRINTS; PR01358; INTRLEUKIN1A.  
DR PRINTS; PR01357; INTRLEUKIN1AB.  
DR ProDom; PD002536; Interleukin\_1; 1.

Query Match 63.9%; Score 53; DB 1; Length 271;  
Best Local Similarity 78.6%; Pred. No. 1.5;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGQDITDFQILENQ 16  
Db 257 GPPSITDFQILENQ 270

## RESULT 15

Q53QF9 HUMAN  
ID Q53QF9 HUMAN PRELIMINARY; PRT; 271 AA.  
AC Q53QF9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein IL1A.  
GN Name=IL1A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Bielicki L., Cedroni M.;  
RT "The sequence of Homo sapiens BAC clone RP11-285D1.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.H.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Wilson R.K.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC112235; AAX93054.1; -; Genomic\_DNA.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006954; P:inflammatory response; IEA.  
KW Hypothetical protein; Inflammatory response; Mitogen; Pyrogen.  
SQ SEQUENCE 271 AA; 30606 MW; CBCC49569D9ED40 CRC64;

Query Match 63.9%; Score 53; DB 2; Length 271;  
Best Local Similarity 78.6%; Pred. No. 1.5;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGQDITDFQILENQ 16  
Db 257 GPPSITDFQILENQ 270

Search completed: January 5, 2006, 21:47:00  
Job time : 237 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 5, 2006, 21:36:41 ; Search time 37 Seconds  
(without alignments)  
41.607 Million cell updates/sec

Title: US-09-894-550-3  
Perfect score: 83  
Sequence: 1 TKGGQDITDFQILENQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	65.1	269	1 ICHUIB	interleukin-1 beta
2	53	63.9	271	1 ICHUIA	interleukin-1 alpha
3	52	62.7	270	2 I46620	interleukin-1 alpha
4	50	60.2	270	1 S10532	interleukin-1 alpha
5	48	57.8	266	1 ICB01B	interleukin-1 beta
6	48	57.8	266	1 S23010	interleukin-1 beta
7	47.5	57.2	214	2 JC5646	interleukin-1 beta
8	44	53.0	727	2 A32561	cadmium-transporter
9	44	53.0	888	2 C40170	glutamate receptor
10	44	53.0	894	2 S49460	glutamate receptor
11	44	53.0	894	2 S50128	glutamate receptor
12	44	53.0	894	2 S53696	glutamate receptor
13	43	51.8	545	2 F86834	alpha-glucosidase
14	42	50.6	231	2 S31693	MADS box protein g
15	42	50.6	267	1 JN0724	interleukin-1 beta
16	42	50.6	267	2 S38373	interleukin-1 beta
17	42	50.6	268	1 A61246	interleukin-1 alpha
18	42	50.6	268	1 ICB01A	interleukin-1 alpha
19	41	49.4	250	2 T31827	hypothetical prote
20	41	49.4	653	2 D69815	conserved hypothet
21	41	49.4	1216	2 T09224	spindle assembly c
22	41	49.4	1697	2 T00079	hypothetical prote
23	40	48.2	135	2 T34125	hypothetical prote
24	40	48.2	227	2 S12378	MADS box protein d
25	40	48.2	238	2 S67594	RAD59 protein - ye
26	40	48.2	300	2 A81418	pseudouridylylate sy
27	40	48.2	319	2 B82381	transcription regu
28	40	48.2	611	2 S09142	ND5 intron 1 prote
29	39	47.0	552	2 T45663	hypothetical prote

ALIGNMENTS

RESULT 1

ICHUIB

interleukin-1 beta precursor [validated] - human  
N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Homo sapiens (man)  
C>Date: 28-Feb-1986 #sequence revision 15-May-1998 #text change 09-Jul-2004  
C/Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19  
R:Clark, B.D.; Collina, L.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.  
Nucleic Acids Res. 14, 7897-7914, 1986

A:Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev  
A:Reference number: A25542; MUID:87040762; PMID:3490654  
A:Accession: A25542

A:Molecule type: DNA; mRNA

A:Residues: 1-5, 'K', 7-269 <CLA>

A:Cross-references: UNIPROT:P01584; UNIPARC:UPI0000030874; GB:X04500; NTD:g33788  
A>Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu

R:Bensi, G.; Raugel, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.  
Gene 52, 95-101, 1987

A:Title: Human interleukin-1 beta gene.

A:Reference number: A29019; MUID:87248099; PMID:2954882

A:Accession: A29019

A:Molecule type: DNA

A:Residues: 1-269 <BEN>

A:Cross-references: UNIPARC:UPI0000054161; GB:M15840; NTD:g186281; PIDN:AAA74137.1; PID

R:Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare

Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984

A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.

A:Reference number: A94023; MUID:85088517; PMID:6083565

A:Accession: A94023

A:Molecule type: mRNA

A:Residues: 1-5, 'K', 7-269 <AUR>

A:Cross-references: UNIPARC:UPI0000030874; GB:X02770; NTD:g186268; PIDN:AAA36106.1; PID

R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.

Nature 315, 641-647, 1985

A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complemen

A:Reference number: A93361; MUID:85240547; PMID:2989698

A:Accession: A93361

A:Molecule type: mRNA

A:Residues: 1-269 <MAR>

A:Cross-references: UNIPARC:UPI0000054161; GB:X02532; NTD:g33789; PIDN:CAA26372.1; PID

A>Note: parts of this sequence, including the amino end of the mature form, were confir

R:Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; A

Adv. Gene Technol. 22, 339-340, 1985

A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.

A:Reference number: I51852

A:Accession: I51852

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEB>

A:Cross-references: UNIPARC:UPI000016AB0A; GB:M54933; NID:g186287; PIDN:AAA59136.1; PID

R:Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hir

Biochem. Biophys. Res. Commun. 143, 345-352, 1987

A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
A;Reference number: I52217; MUID:87156769; PMID:3493774  
A;Accession: I65200  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-269 <NIS>  
A;Cross-references: UNIPARC:UPI0000054161; GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:  
R;Kotenko, S.V.; Bulenikov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov,  
ii, S.A.; Vinetskii, Y.P.  
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin  
A;Reference number: I38131; MUID:90249285; PMID:2635664  
A;Accession: I38132  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-269 <KOT>  
A;Cross-references: UNIPARC:UPI0000054161; EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:  
R;Zsabo, K.M.; Wypych, J.; Yuschenskoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.  
Blood 71, 962-968, 1988  
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic  
A;Reference number: A90732; MUID:88184226; PMID:3281727  
A;Accession: B27616  
A;Molecule type: protein  
A;Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>  
A;Cross-references: UNIPARC:UPI000017367D  
R;Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.  
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
A;Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines  
A;Reference number: A48293; MUID:93348250; PMID:8346241  
A;Contents: annotation; myristylation of lysines  
R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
Biochim. Biophys. Acta 1118, 25-35, 1991  
A;Title: The role of arginine residues in interleukin 1 receptor binding.  
A;Reference number: S19608; MUID:92110334; PMID:1837236  
A;Contents: annotation; type 1 IL-1 receptor interaction site  
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
R;Clare, G.M.; Gronenborn, A.M.  
submitted to the Brookhaven Protein Data Bank, January 1991  
A;Reference number: A50049; PDB:1i1B  
A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
R;Clare, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
Biochemistry 30, 2315-2323, 1991  
A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution by  
A;Reference number: A44675; MUID:91159409; PMID:2001363  
A;Contents: annotation; (1)H-NMR structural determination  
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
J. Biol. Chem. 266, 7081-7086, 1991  
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a con  
A;Reference number: A39774; MUID:91201363; PMID:2016316  
A;Contents: annotation  
R;Finzel, B.C.; Watenpugh, K.D.; Einspahr, H.M.  
submitted to the Brookhaven Protein Data Bank, December 1989  
A;Reference number: A50016; PDB:1i1B  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms  
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpugh, K.D.; Einspahr,  
J. Mol. Biol. 209, 779-791, 1989  
A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolu  
A;Reference number: A44666; MUID:90064532; PMID:2585509  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms  
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag  
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.  
C;Comment: Interleukin-beta precursor is less heavily myristoylated than interleukin-1a  
C;Genetics:  
A;Gene: GDB: IL1B  
A;Cross-references: GDB:I20094; OMIM:I47720  
A;Map position: 2q13-2q21  
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3  
C;Superfamily: interleukin-1  
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag  
F;17-269/Product: interleukin-1 beta #status experimental <il1>  
F;176/Binding site: myristate (lys) (covalent) #status experimental  
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 65.1%; Score 54; DB 1; Length 269;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TKGGQDITDF 10  
|||||  
Db 253 TKGGQDITDF 262  
|||||  
RESULT 2  
ICHUIA  
interleukin-1 alpha precursor - human  
N;Alternate names: hematopoietin-1; IL-1 alpha  
C;Species: Homo sapiens (man)  
C;Date: 28-Feb-1986 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: A23385; A24073; I55959; I52217; A01847; A27616; I38131; S19608  
R;Furutani, Y.; Notake, M.; Fukui, T.; Ohue, M.; Nomura, H.; Yamada, M.; Nakamura, S.  
Nucleic Acids Res. 14, 3167-3179, 1986  
A;Reference number: A23385; MUID:86205226; PMID:3486405  
A;Accession: A23385  
A;Molecule type: DNA  
A;Residues: 1-271 <FUR>  
A;Cross-references: UNIPROT:P01583; UNIPARC:UPI00001563D5; GB:X03833; NID:g33785; PIDN:  
R;Furutani, Y.; Notake, M.; Yamayoshi, M.; Yamagishi, J.I.; Nomura, H.; Ohue, M.; Furuta  
Nucleic Acids Res. 13, 5869-5882, 1985  
A;Reference number: A93581; MUID:85297782; PMID:2994016  
A;Accession: A24073  
A;Molecule type: mRNA  
A;Residues: 1-271 <FUR>  
A;Cross-references: UNIPARC:UPI00001563D5; GB:X02851; NID:g33794; PIDN:CAA26604.1; PID:  
R;Gubler, U.; Chua, A.O.; Stern, A.S.; Hellmann, C.P.; Vitek, M.P.; Dechiara, T.M.; Benj  
L.; Stremlo, D.; Wittreich, B.H.; Woehle, D.; Mizek, S.B.; Lomedico, P.T.  
J. Immunol. 136, 2492-2497, 1986  
A;Title: Recombinant human interleukin 1 alpha: purification and biological characteriza  
A;Reference number: I55959; MUID:86141855; PMID:3485152  
A;Accession: I55959  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-113, 'A', 115-271 <RES>  
A;Cross-references: UNIPARC:UPI00000000CCF; GB:M28983; NID:g186279; PIDN:AAA59134.1; PID:  
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Masui, Y.; Nakai, S.; Hira  
Biochem. Biophys. Res. Commun. 143, 345-352, 1987  
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
A;Reference number: I52217; MUID:87156769; PMID:3493774  
A;Accession: I52217  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-113, 'A', 115-271 <RE2>  
A;Cross-references: UNIPARC:UPI00000000CCF; GB:M15329; NID:g186277; PIDN:AAA59133.1; PID:  
R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.  
Nature 315, 641-647, 1985  
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complement  
A;Reference number: A93361; MUID:85240547; PMID:2989698  
A;Accession: A01847  
A;Molecule type: mRNA  
A;Residues: 1-113, 'A', 115-271 <MAR>  
A;Cross-references: UNIPARC:UPI00000000CCF; GB:X02531; NID:g33787; PIDN:CAA26371.1; PID:  
A;Note: the degree of similarity among the IL-1 precursors suggests that the amino ends  
A;Note: the lack of a specific hydrophobic segment in the precursor sequence suggests th  
proteins  
R;Zsabo, K.M.; Wypych, J.; Yuschenskoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.  
Blood 71, 962-968, 1988  
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic  
A;Reference number: A90732; MUID:88184226; PMID:3281727  
A;Accession: A27616  
A;Molecule type: protein  
A;Residues: 113, 'A', 115-119, 121-127, 'X', 129-132 <ZSE>  
A;Cross-references: UNIPARC:UPI000017367C  
R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
Biochim. Biophys. Acta 1118, 25-35, 1991  
A;Title: The role of arginine residues in interleukin 1 receptor binding.  
A;Reference number: S19608; MUID:92110334; PMID:1837236  
A;Contents: annotation; type 1 IL-1 receptor interaction site

A>Note: modification of Arg-118 by phenylglyoxal blocks receptor binding  
 R:Kotenko, S.V.; Bulenikov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, I.I.; S.A.; Vinetskii, Y.P.  
 Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
 A:Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta]  
 A:Reference number: 138131; MUID:90249285; PMID:2635664  
 A:Accession: 138131  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-113, 'A', 115-271 <RE3>  
 A:Cross-references: UNIPARC:UPI00000000CF; EMBL:X56086; NID:G35660; PIDN:CAA39566.1; PID:113-271/Domain: propeptide #status predicted <PRO>  
 R:Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
 A:Title: The 31-kDa precursor of interleukin-1 alpha is myristoylated on specific lysines  
 A:Reference number: A48293; MUID:93348250; PMID:8346241  
 A:Contents: annotation; myristylation of lysines  
 R:Hayada, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
 J. Biol. Chem. 266, 7081-7086, 1991  
 A:Title: Structure-function mapping of interleukin-1 precursors. Cleavage leads to a conformationally active fragment  
 A:Reference number: A39774; MUID:91201363; PMID:2016316  
 A:Contents: annotation  
 C:Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte proliferation  
 C:Comment: IL-1 proteins are involved in the inflammatory response, being identified as IL-1s.  
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-1alpha, unlike interleukin-1beta, is fully active.  
 C:Comment: Lys-83 is myristoylated more heavily than Lys-82. About 10-15% of the IL-1alpha is myristoylated.  
 C:Genetics:  
 A:Gene: GDB:IL1A  
 A:Cross-references: GDB:120695; OMIM:147760  
 A:Map position: 2q13-2q21  
 A:Introns: 16/2; 32/3; 107/1; 164/1; 205/3  
 C:Superfamily: interleukin-1  
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage  
 F:112/Domain: propeptide #status predicted <PRO>  
 F:113-271/Product: interleukin-1 alpha #status predicted <IL1>  
 F:82,83/Binding site: myristate (Lys) (covalent) (partial) #status experimental  
 Query Match 63.9%; Score 53; DB 1; Length 271;  
 Best Local Similarity 78.6%; Pred. No. 0.17; Mismatches 3; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;  
 QY 3 GGQDITDFQILENQ 16  
 Db 257 GGLPSVTDFOILENQ 270  
 RESULT 3  
 I46620  
 interleukin-1 alpha precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C:Accession: I46620  
 R:Maliszewski, C.  
 Nucleic Acids Res. 14, 4282, 1990  
 A:Title: Nucleotide sequence of porcine interleukin-1 alpha.  
 A:Reference number: I46620  
 A:Accession: I46620  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-270 <MAL>  
 A:Cross-references: UNIPROT:P18430; UNIPARC:UPI000014F113; GB:M86730; NID:G164622; PIDN:113-271/Domain: propeptide #status predicted <PRO>  
 C:Superfamily: interleukin-1  
 C:Keywords: lipoprotein; myristylation  
 F:112/Domain: propeptide #status predicted <PRO>  
 F:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
 F:82,83/Binding site: myristate (Lys) (covalent) #status predicted  
 Query Match 62.7%; Score 52; DB 2; Length 270;  
 Best Local Similarity 66.7%; Pred. No. 0.25; Mismatches 2; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;

QY 2 KGGQDITDFQILENQ 16  
 Db 255 RGLPSVTDFOILENQ 269

## RESULT 4

S10532  
 interleukin-1 alpha precursor - pig  
 N:Alternate names: hematopoietin-1; IL-1 alpha  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 20-Feb-1995 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
 C:Accession: S10532  
 R:Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.  
 Nucleic Acids Res. 18, 4282, 1990  
 A:Title: Porcine IL-1 alpha cDNA nucleotide sequence.  
 A:Reference number: S10532; MUID:90332454; PMID:2377484  
 A:Accession: S10532  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-270 <MAL>  
 A:Cross-references: UNIPROT:P18430; UNIPARC:UPI000012D493; EMBL:X52731; NID:G1987; PIDN:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
 C:Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte proliferation  
 C:Comment: IL-1 proteins are involved in the inflammatory response, being identified as IL-1s.  
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-1alpha, unlike interleukin-1beta, is fully active.  
 C:Superfamily: interleukin-1  
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage  
 F:112/Domain: propeptide #status predicted <PRO>  
 F:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
 F:82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 60.2%; Score 50; DB 1; Length 270;  
 Best Local Similarity 71.4%; Pred. No. 0.55; Mismatches 1; Indels 0; Gaps 0;  
 Matches 10; Conservative 1;

QY 3 GGQDITDFQILENQ 16  
 Db 256 GLPSVTDFOILENQ 269

## RESULT 5

ICB01B  
 interleukin-1 beta precursor - bovine  
 N:Alternate names: hematopoietin-1; IL-1 beta  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C:Accession: J10010; S01380  
 R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Melnick, J.L.  
 Mol. Immunol. 25, 429-437, 1988  
 A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin 1-beta.  
 A:Reference number: A94695; MUID:88318652; PMID:3261832  
 A:Accession: J10010  
 A:Molecule type: mRNA  
 A:Residues: 1-266 <MAL>  
 A:Cross-references: UNIPROT:P09428; UNIPARC:UPI0000167C08; GB:M37211; NID:G163200; PIDN:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
 C:Superfamily: interleukin-1  
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage; mitogen  
 F:112/Domain: propeptide #status predicted <PRO>  
 F:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
 F:82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 62.7%; Score 52; DB 2; Length 270;  
 Best Local Similarity 66.7%; Pred. No. 0.25; Mismatches 2; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;

QY 3 GGQDITDFQILENQ 16  
 Db 257 GGLPSVTDFOILENQ 270  
 RESULT 3  
 I46620  
 interleukin-1 alpha precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C:Accession: I46620  
 R:Maliszewski, C.  
 Nucleic Acids Res. 14, 4282, 1990  
 A:Title: Nucleotide sequence of porcine interleukin-1 alpha.  
 A:Reference number: I46620  
 A:Accession: I46620  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-270 <MAL>  
 A:Cross-references: UNIPROT:P18430; UNIPARC:UPI000014F113; GB:M86730; NID:G164622; PIDN:113-271/Domain: propeptide #status predicted <PRO>  
 C:Superfamily: interleukin-1  
 C:Keywords: lipoprotein; myristylation  
 F:112/Domain: propeptide #status predicted <PRO>  
 F:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
 F:82,83/Binding site: myristate (Lys) (covalent) #status predicted  
 Query Match 62.7%; Score 52; DB 2; Length 270;  
 Best Local Similarity 66.7%; Pred. No. 0.25; Mismatches 2; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;

```

Query Match      57.8%; Score 48; DB 1; Length 266;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KGGQDITDFQI 12
       :|||||:
Db      251 RGGQDITDFRM 261

RESULT 6
S23010
interleukin-1 beta precursor - sheep
N;Alternate names: hematoopoietin-1, IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S23010; S43047; S13092; B61246
R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A;Reference number: S23010; MUID:92119335; PMID:1840515
A;Accession: S23010
A;Molecule type: mRNA
A;Residues: 1-266 <SEO>
A;Cross-references: UNIPROT:P21621; UNIPARC:UPI0000030876; EMBL:X56972; NID:gl808; PIDN:
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an addi
R;Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A;Reference number: S43047
A;Accession: S43047
A;Molecule type: mRNA
A;Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'L', 146-266 <SAR>
A;Cross-references: UNIPARC:UPI000016C4C5; EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:
R;Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A;Title: Nucleotide sequence of ovine interleukin-1 beta.
A;Reference number: S13092; MUID:91088326; PMID:2263490
A;Accession: S13092
A;Molecule type: mRNA
A;Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <FIS>
A;Cross-references: UNIPARC:UPI000017367E; EMBL:X54796
A;Note: the authors translated the codon AGT for residue 62 as Arg
R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A;Reference number: A61246; MUID:92120716; PMID:1769692
A;Accession: B61246
A;Molecule type: mRNA
A;Residues: 1-144, 'L', 146-266 <AND>
A;Cross-references: UNIPARC:UPI000002CD35
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
F;114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match      57.8%; Score 48; DB 1; Length 266;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KGGQDITDFQI 12
       :|||||:
Db      251 RGGQDITDFRM 261

RESULT 7
JC5646
interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: JC5646

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R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa, A
Gene 177, 11-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-1 b
A;Reference number: JC5646; MUID:97080493; PMID:8921838
A;Accession: JC5646
A;Molecule type: mRNA
A;Residues: 1-214 <KAT>
A;Cross-references: UNIPROT:Q28386; UNIPARC:UPI000002ABD0; DBJ:D42165; NID:g2463549; PI
C;Comment: This protein mediates a variety of physiological response to infections and i
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce
C;Superfamily: interleukin-1

Query Match      57.2%; Score 47.5; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy      1 TKGQDITDFQILE 14
       :|||:|||||:|
Db      198 TRGRDITDF-IME 210

RESULT 8
A32561
cadmium-transporting ATPase (EC 3.6.1.-) [validated] - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A32561
R;Nucifora, G.; Chu, L.; Miera, T.K.; Silver, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 3544-3548, 1989
A;Title: Cadmium resistance from Staphylococcus aureus plasmid pI258 cada gene results f
A;Reference number: A94225; MUID:89284460; PMID:2524829
A;Accession: A32561
A;Molecule type: DNA
A;Residues: 1-727 <NUC>
A;Cross-references: UNIPROT:P20021; UNIPARC:UPI0000126DA5
C;Genetics:
A;Gene: cada
C;Function:
A;Description: EC 3.6.1.-; cadmium-transporting ATPase [validated, MUID:89264460]; respon
C;Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding
C;Keywords: hydrolase; phosphoprotein
F;18-47/Domain: heavy-metal-associated homology <HMA1>
F;134-461/Domain: ATPase transduction domain homology <ATP>
F;542-686/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match      53.0%; Score 44; DB 2; Length 727;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 TKGQDITDFQILENQ 16
       :|||:|||||:|
Db      421 TKGVPVVTDFEVLNDQ 436

RESULT 9
C40170
glutamate receptor C precursor - rat
N;Alternate names: glutamate receptor 3; glutamate receptor K3 chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Aug-1992 #sequence_revision 18-Sep-1992 #text_change 31-Dec-2004
C;Accession: C40170; JH0311; B40171
R;Keinonen, K.; Wisden, W.; Sommer, B.; Werner, P.; Herb, A.; Verdoorn, T.A.; Sakmann,
Science 249, 556-560, 1990
A;Title: A family of AMPA-selective glutamate receptors.
A;Reference number: A40170; MUID:90341779; PMID:2166337
A;Accession: C40170
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-888 <KEI>
A;Cross-references: UNIPROT:P19492; UNIPARC:UPI0000033423; GB:M36420; NID:g204397; PIDN:
R;Nakanishi, N.; Schneider, N.A.; Axel, R.
Neuron 5, 569-581, 1990
A;Title: A family of glutamate receptor genes: evidence for the formation of heteromult

```

A;Reference number: JH0310; MUID:91026040; PMID:1699567  
A;Accession: JH0311  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-769; TP, 772-779, 'S', 781-783, 'I', 785-800, 'AKDSG', 806-888 <NAK>  
A;Cross-references: UNIPARC:UPI000002AA92; GB:X54656; NID:g56291; PIDN:CAA38466.1; PID:g56291  
R;Boulter, J.; Hollmann, M.; O'Shea-Greenfield, A.; Hartley, M.; Deneris, E.; Maron, C.; Science 249, 1033-1037, 1990  
A;Title: Molecular cloning and functional expression of glutamate receptor subunit genes  
A;Reference number: A40171; MUID:90371298; PMID:2168579  
A;Accession: B40171  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-293, 'S', 295-342, 'C', 344-393, 'S', 395-516, 'NA', 519-692, 694-792, 794-888 <BOU>  
A;Cross-references: UNIPARC:UPI0000177955; GB:M85036  
C;Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor hom  
C;Keywords: alternative splicing; neurotransmitter receptor; transmembrane protein  
P;421-851/Domain: glutamate receptor homology <GRH>  
  
Query Match 53.0%; Score 44; DB 2; Length 888;  
Best Local Similarity 57.1%; Pred. No. 23;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 GGQDITDFQILENQ 16  
|||:|||||:|  
Db 257 GGANITGFQIVNNE 270  
  
RESULT 10  
S49460  
glutamate receptor chain GluR3 - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 31-Dec-2004  
C;Accession: S49460  
R;McLaughlin, D.P.; Kerwin, R.W.  
submitted to the EMBL Data Library, October 1994  
A;Reference number: S49460  
A;Accession: S49460  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-894 <MCL>  
A;Cross-references: UNIPROT:P42263; UNIPARC:UPI0000033427; EMBL:X82068; NID:g558587; PID  
C;Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor hom  
C;Keywords: neurotransmitter receptor  
P;427-857/Domain: glutamate receptor homology <GRH>  
  
Query Match 53.0%; Score 44; DB 2; Length 894;  
Best Local Similarity 57.1%; Pred. No. 23;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 GGQDITDFQILENQ 16  
|||:|||||:|  
Db 263 GGANITGFQIVNNE 276  
  
RESULT 11  
S50128  
glutamate receptor 3 isoform flip - human  
N;Alternate names: AMPA receptor chain GluR3 isoform flip  
C;Species: Homo sapiens (man)  
C;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 31-Dec-2004  
C;Accession: S50128  
R;Rampersad, V.; Elliott, C.E.; Nutt, S.L.; Foldes, R.L.; Kamboj, R.K.  
Biochim. Biophys. Acta 1219, 563-566, 1994  
A;Title: Human glutamate receptor hGluR3 flip and flop isoforms: cloning and sequencing  
A;Reference number: S50128; MUID:95002179; PMID:7918660  
A;Accession: S50128  
A;Molecule type: mRNA  
A;Residues: 1-894 <RAM>  
A;Cross-references: UNIPROT:Q9CF03; UNIPARC:UPI000002AA91; EMBL:U10301; NID:g507826; PID  
C;Superfamily: alpha-glucosidase; alpha-amylase core homology  
C;Genetics:  
A;Gene: GluR3-flip  
A;Map position: X

C;Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor homo  
C;Keywords: alternative splicing; ion channel; neurotransmitter receptor; transmembrane  
P;427-857/Domain: glutamate receptor homology <GRH>  
  
Query Match 53.0%; Score 44; DB 2; Length 894;  
Best Local Similarity 57.1%; Pred. No. 23;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 GGQDITDFQILENQ 16  
|||:|||||:|  
Db 263 GGANITGFQIVNNE 276  
  
RESULT 12  
S53696  
glutamate receptor 3 isoform flop - human  
N;Alternate names: AMPA receptor chain GluR3 isoform flop  
C;Species: Homo sapiens (man)  
C;Date: 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 31-Dec-2004  
C;Accession: S53696; S50129  
R;Rampersad, V.; Elliott, C.E.; Nutt, S.L.; Foldes, R.L.; Kamboj, R.K.  
submitted to the EMBL Data Library, June 1994  
A;Description: Human glutamate receptor hGluR3 flip and flop isoforms: cloning and sequ  
A;Reference number: S53696  
A;Accession: S53696  
A;Molecule type: mRNA  
A;Residues: 1-894 <RAM>  
A;Cross-references: UNIPROT:P42263; UNIPARC:UPI000012B7C6; EMBL:U10302; NID:g507828; PID  
R;Rampersad, V.; Elliott, C.E.; Nutt, S.L.; Foldes, R.L.; Kamboj, R.K.  
Biochim. Biophys. Acta 1219, 563-566, 1994  
A;Title: Human glutamate receptor hGluR3 flip and flop isoforms: cloning and sequencing  
A;Reference number: S50128; MUID:95002179; PMID:7918660  
A;Accession: S50129  
A;Molecule type: mRNA  
A;Residues: 776-813 <RAW>  
A;Cross-references: UNIPARC:UPI0000177952; EMBL:U10302  
C;Genetics:  
A;Gene: GluR3-flip  
A;Map position: X  
C;Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor hom  
C;Keywords: alternative splicing; ion channel; neurotransmitter receptor; transmembrane  
P;427-857/Domain: glutamate receptor homology <GRH>  
  
Query Match 53.0%; Score 44; DB 2; Length 894;  
Best Local Similarity 57.1%; Pred. No. 23;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 GGQDITDFQILENQ 16  
|||:|||||:|  
Db 263 GGANITGFQIVNNE 276  
  
RESULT 13  
F86834  
alpha-glucosidase (EC 3.2.1.20) [imported] - Lactococcus lactis subsp. lactis (strain II  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: F86834  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrh  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: F86834  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-545 <STO>  
A;Cross-references: UNIPROT:Q9CF03; UNIPARC:UPI00000C6AC5; GB:AE005176; PID:gl2724692; i  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: agl  
C;Superfamily: alpha-glucosidase; alpha-amylase core homology  
C;Keywords: glycosidase; hydrolase

```
Query Match          51.8%; Score 43; DB 2; Length 545;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGQDITDFQILE 14
Db 64 GGYDISDVQVID 75

RESULT 14
S31693
MADS box protein gp - garden petunia
N;Alternate names: floral homeotic protein gp; transcription factor gp
C;Species: Petunia x hybrida (garden petunia)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31693
R;Kush, A.; Brunelle, A.; Shevell, D.; Chua, N.H.
submitted to the EMBL Data Library, November 1992
A;Description: Nucleotide sequence and expression pattern of two genes encoding MADS box
A;Reference number: S31693
A;Accession: S31693
A;Molecule type: mRNA
A;Residues: 1-231 <KUS>
A;Cross-references: UNIPROT:Q07472; UNIPARC:UPI000012BB11; EMBL:X69946; NID:G22664; PID:
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match          50.6%; Score 42; DB 2; Length 231;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGQDITDFQILE 14
Db 220 GGSDDITTFALLE 231

RESULT 15
JN0724
interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: JN0724
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be
A;Reference number: JN0724; MUID:93314975; PMID:8325511
A;Accession: JN0724
A;Molecule type: mRNA
A;Residues: 1-267 <HUE>
A;Cross-references: UNIPROT:P26889; UNIPARC:UPI0000030879; GB:M86725; NID:gl64607; PIDN:
A;Experimental source: alveolar macrophage
C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processes i
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;115-267/Product: interleukin-1 beta #status predicted <IL1>
F;77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match          50.6%; Score 42; DB 1; Length 267;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
Db 251 SKGRQDITDF 260

Search completed: January 5, 2006, 21:47:43
Job time : 38 secs
```



CC relates to a novel method for obtaining a dual-specificity antibody that  
 CC specifically binds two different but structurally related molecules. The  
 CC dual specificity antibody which specifically binds to IL-1alpha/IL-1beta  
 CC is useful for detecting IL-1alpha or IL-1beta in an in vitro biological  
 CC sample or tissue, for diagnostic purposes. The antibody is also useful  
 CC for inhibiting IL-1alpha or IL-1beta activity in vitro and for treating  
 CC IL-1-related disorder e.g. inflammatory disorder or autoimmune disorder  
 CC selected from rheumatoid arthritis, Crohn's disease, multiple sclerosis,  
 CC insulin-dependent diabetes mellitus and psoriasis. A dual specificity  
 CC antibody of the invention is useful for blocking the functions of more  
 CC than one member of the protein family that can be beneficial for  
 CC alleviating disease symptoms or for interrupting the disease process  
 CC itself, to detect structurally related antigens, to purify structurally  
 CC related antigens and in diagnostic assays involving the antigens. A dual  
 CC specificity antibody is also useful for treating diseases of the central  
 CC nervous system, acute and chronic pain, lipid imbalance, and inflammation  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDFQILENQ 16  
 |||||  
 Db 1 TKGGQDITDFQILENQ 16

## RESULT 2

AAW95365  
 ID AAW95365 standard; protein; 271 AA.

XX AC AAW95365;

XX DT 26-MAR-1999 (first entry)

XX DE Macaca interleukin (IL)-1 alpha precursor polypeptide.

XX KW Interleukin; IL-1 alpha propiece; apoptosis; variant; malignant; cancer;  
 XX cell death.

XX OS Macaca sp.

XX PN W09854205-A1.

XX PD 03-DEC-1998.

XX PF 28-MAY-1998; 98WO-US010839.

XX PR 30-MAY-1997; 97US-0048137P.

XX PR 27-MAY-1998; 98US-0065647P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Pollock AS, Lovett DH, Turck J;

XX DR WPI; 1999-059804/05.

XX PT New polypeptides comprising an apoptosis-inducing domain and a  
 PT heterologous nuclear localisation sequence - useful for, e.g. forming  
 PT compositions and methods for selectively inducing apoptosis in cancer  
 PT cells.

XX PS Disclosure; Page 69; 89pp; English.

XX CC The invention relates to a human interleukin (IL)-1 alpha propiece  
 CC polypeptide. The polypeptide has activity in the selective induction of  
 CC apoptosis in cancer cells. The IL-1 alpha propiece polypeptide or its  
 CC variants which retain the apoptosis-inducing activity are used in  
 CC compositions and methods to selectively induce apoptosis in cancer cells,  
 CC especially malignant cancer cells. The polypeptides form the basis for  
 CC effective, apoptotic-based chemotherapy where apoptosis-inducing agents  
 CC selectively trigger cell death in cancerous cells, but do not harm

CC surrounding normal tissue. The present sequence represents a macaca IL-1  
 CC alpha precursor polypeptide. The IL-1 alpha propiece polypeptides of non-  
 CC human origin can be derived from such precursor polypeptides  
 XX  
 SQ Sequence 271 AA;

Query Match 67.5%; Score 56; DB 2; Length 271;  
 Best Local Similarity 80.0%; Pred. No. 0.32;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KGGQDITDFQILENQ 16  
 |||||  
 Db 256 KGLPSITDFQILENQ 270

## RESULT 3

AAW95362  
 ID AAW95362 standard; protein; 271 AA.

XX AC AAW95362;

XX DT 27-AUG-2003 (revised)

XX DT 26-MAR-1999 (first entry)

XX DE Interleukin (IL)-1 alpha precursor polypeptide from Cercopithecus sp.

XX KW Interleukin; IL-1 alpha propiece; apoptosis; variant; malignant; cancer;  
 XX cell death.

XX OS Cercopithecus torquatus atys.

XX PN W09854205-A1.

XX PD 03-DEC-1998.

XX PF 28-MAY-1998; 98WO-US010839.

XX PR 30-MAY-1997; 97US-0048137P.

XX PR 27-MAY-1998; 98US-0065647P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Pollock AS, Lovett DH, Turck J;

XX DR WPI; 1999-059804/05.

XX PT New polypeptides comprising an apoptosis-inducing domain and a  
 PT heterologous nuclear localisation sequence - useful for, e.g. forming  
 PT compositions and methods for selectively inducing apoptosis in cancer  
 PT cells.

XX PS Disclosure; Page 67-68; 88pp; English.

XX CC The invention relates to a human interleukin (IL)-1 alpha propiece  
 CC polypeptide. The polypeptide has activity in the selective induction of  
 CC apoptosis in cancer cells. The IL-1 alpha propiece polypeptide or its  
 CC variants which retain the apoptosis-inducing activity are used in  
 CC compositions and methods to selectively induce apoptosis in cancer cells,  
 CC especially malignant cancer cells. The polypeptides form the basis for  
 CC effective, apoptotic-based chemotherapy where apoptosis-inducing agents  
 CC selectively trigger cell death in cancerous cells, but do not harm  
 CC surrounding normal tissue. The present sequence represents a IL-1 alpha  
 CC precursor polypeptide from Cercopithecus troquatus atys. The IL-1 alpha  
 CC propiece polypeptides of non-human origin can be derived from such  
 CC precursor polypeptides. (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 271 AA;

Query Match 67.5%; Score 56; DB 2; Length 271;  
 Best Local Similarity 80.0%; Pred. No. 0.32;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KGGQDITDFQILENQ 16





```

Db      115 TKGGQDITDF 124
|||||
RESULT 6
AAR15435
ID   AAR15435 standard; protein; 148 AA.
XX
AC   AAR15435;
XX
XX   25-MAR-2003 (revised)
DT   10-MAR-2003 (revised)
DT   27-FEB-1992 (first entry)
XX
DE   Interleukin-1 beta derivative with amino acids 148 to 153 deleted.
XX
XX   IL-1; [1-148]IL-1 beta; interleukin 6 inducer.
XX
XX   Homo sapiens.
XX
XX   JP03197433-A.
XX
XX   28-AUG-1991.
XX
XX   26-DEC-1989; 89JP-00338998.
XX
XX   26-DEC-1989; 89JP-00338998.
XX
XX   (SAKA ) OTSUKA PHARM CO LTD.
XX
XX   WPI; 1991-356562/49.
XX
XX   IL-6 production inducer - is deriv. of modified amino acid sequence obt'd.
XX   by modification of interleukin I alpha.
XX
XX   Claim 2; Page 2; 17pp; Japanese.
XX
XX   This peptide is a preferred example of an IL-1 beta derivative with IL-6
XX   (inducing activity. Amino acids Gln(149)-Phe((150)-Val(151) - Ser(152) -
XX   Ser(153) have been deleted. The invention covers IL-1 beta deriv.s from
XX   which all or part of the sequence Lys(103) to Ser(153) has been deleted.
XX   (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX   to correct PA field.)
XX
XX   Sequence 148 AA;
Query Match      65.1%; Score 54; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TKGGQDITDF 10
Db      137 TKGGQDITDF 146
|||||
RESULT 7
AAR47552
ID   AAR47552 standard; protein; 150 AA.
XX
AC   AAR47552;
XX
XX   25-MAR-2003 (revised)
DT   21-JUL-1994 (first entry)
XX
XX   Sequence of human interleukin-1-beta (IL-1-beta) deletion mutant delta
XX   SND.
XX
XX   Interleukin-1-beta; deletion mutant; delta SND.
XX
XX   Homo sapiens.
XX
XX   WO9400491-A1.
XX

PD      06-JAN-1994.
XX
XX   23-JUN-1993; 93WO-SR000562.
XX
XX   25-JUN-1992; 92SE-00001966.
XX
XX   (TRIO-) TRION FORSKNING OCH UTVECKLING AB.
XX
XX   Bartfai T, Bristulf J, Cserzoe M, Pongor S, Simoncsits A;
XX   Tjoernhammar M;
XX   WPI; 1994-026152/03.
XX   N-PSDB; AAQ54001.
XX
XX   New interleukin-1 beta deletion mutants - used as carriers or adjuvants
XX   for active agents or as therapeutic and/or prophylactic agents.
XX
XX   Disclosure; Table 3, page 14; 26pp; English.
XX
XX   The human IL-1-beta gene was purchased from British Bio-technology
XX   (BBG25). It was subcloned into M13mp18 and subjected to oligo- directed
XX   in vitro mutagenesis. The rDNA obt'd. was cloned into an expression vector
XX   and used to transform E.coli JM101 cells to obtain the deletion mutant
XX   delta SND which has Ser-Aan-Asp at posns. 52-54 of human IL-1-beta
XX   deleted (AAQ54001/R47552). In a test for pyrogenic effects in rabbits,
XX   delta SND evoked lower fever reactions than those caused by the same,
XX   doses of IL-1-beta. Delta SND binds with the same high affinity to IL-1
XX   receptors (tupe II) on human Raji cells as does IL-1-beta. Delta SND
XX   binds with a 10-fold less affinity to IL-1 receptors (type I) on mouse E1
XX   -4 thymoma cells. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX   Sequence 150 AA;
Query Match      65.1%; Score 54; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TKGGQDITDF 10
Db      134 TKGGQDITDF 143
|||||
RESULT 8
ABR83162
ID   ABR83162 standard; protein; 150 AA.
XX
AC   ABR83162;
XX
XX   15-JAN-2004 (first entry)
XX
XX   Human mature IL-1beta sequence.
XX
XX   Hu007; analogue; humanized antibody; IL-1beta; interleukin-1 beta;
XX   complementarity determining region; osteopathic; antiarthritic;
XX   gene therapy; CDR; human.
XX
XX   Homo sapiens.
XX
XX   WO2003073982-A2.
XX
XX   12-SEP-2003.
XX
XX   20-FEB-2003; 2003WO-US0003117.
XX
XX   28-FEB-2002; 2002US-0361423P.
XX
XX   (ELIL ) LILLY & CO ELI.
XX
XX   Beals JM, Huang L, Lu J, Rogers DP, Witcher DR;
XX   WPI; 2003-731644/69.
XX
XX   New analog of humanized antibody Hu007 that specifically binds mature IL-

```

PT 1 beta, useful for the manufacture of a medicament for treating  
PT rheumatoid arthritis or osteoarthritis.

PS Disclosure; Fig 3; 120pp; English.

XX The invention relates to an analogue of humanized antibody Hu007 that  
XX specifically binds mature IL-1beta and comprises at least one amino acid  
CC substitution at positions 54, 55 or 56 of the heavy chain complementarity  
CC determining region 2 (CDR2). The analogue is useful for the manufacture  
CC of a medicament for treating rheumatoid arthritis or osteoarthritis or  
CC for inhibiting cartilage destruction. The present sequence represents a  
CC human interleukin-1beta (IL-1beta) mature sequence

XX Sequence 150 AA;

Query Match 65.1%; Score 54; DB 7; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10  
| | | | | | | |  
Db 137 TKGQDITDF 146

RESULT 9  
AAM47924  
ID AAM47924 standard; protein; 151 AA.

AC AAM47924;

DT 26-FEB-2002 (first entry)

DE Human IL-1beta.

KW Human; IL-1 beta gene; IL-1M; IL-1beta; gene.

OS Homo sapiens.

PN CN1307138-A.

PD 08-AUG-2001.

PF 28-JAN-2000; 2000CN-00100695.

PR 28-JAN-2000; 2000CN-00100695.

PA (PREC-) PRECLINICAL MEDICINE INST MILITARY ACAD.

PI Ling S, Song X;

DR WPI; 2002-026898/04.

DR N-PSDB; ABA05394.

XX Expression vector pBVIL1 comprising modified human IL-1 beta gene IL-1M  
PT and endoenzyme sites, useful for antigen expression.

PS Claim 5; Fig 2; 22pp; Chinese.

XX The invention relates to an expression vector with total length 4118 base  
CC pairs (bp; sequence not defined) and including the great part of plasmid  
CC pBV220 and modified human IL-1 beta gene IL-1M, which contains start  
CC codon ATG, stop codon TAA and endoenzyme sites XhoI and XbaI. Owing to  
CC the low non-specific reaction of the pBVIL1 expressed fusion protein, the  
CC immunological adjuvant function of IL-1M active peptide and the cloning  
CC site of foreign gene with complementary enzyme for gene linkage, the  
CC pBVIL1 is ideal vector for antigen expression and may be applied widely.  
CC The present sequence is that of human IL-1beta of the invention

XX Sequence 151 AA;

Query Match 65.1%; Score 54; DB 5; Length 151;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10  
| | | | | | | |  
Db 135 TKGQDITDF 144

RESULT 10  
AAR15434  
ID AAR15434 standard; protein; 152 AA.

AC AAR15434;

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 27-FEB-1992 (first entry)

XX Interleukin-1 beta derivative with Arg(4) deleted.

XX IL-1; des4Arg IL-1 beta; interleukin 6 inducer.

OS Homo sapiens.

OS Synthetic.

PN JP03197433-A.

PD 28-AUG-1991.

PF 26-DEC-1989; 89JP-00338998.

PR 26-DEC-1989; 89JP-00338998.

PA (SAKA) OTSUKA PHARM CO LTD.

XX WPI; 1991-356562/49.

XX IL-6 production inducer - is deriv. of modified amino acid sequence obtd.  
PT by modification of interleukin I alpha.

PS Claim 2; Page 2; 17pp; Japanese.

XX This peptide is a preferred example of an IL-1 beta derivative with IL-6  
CC inducing activity. Arg at position 4 is deleted. (Updated on 10-MAR-2003  
CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 152 AA;

Query Match 65.1%; Score 54; DB 2; Length 152;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10  
| | | | | | | |  
Db 136 TKGQDITDF 145

RESULT 11  
AAR15746  
ID AAR15746 standard; protein; 152 AA.

AC AAR15746;

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 27-FEB-1992 (first entry)

XX Interleukin-1 beta derivative with Arg(98) deleted.

XX IL-1; [des98Arg] IL-1 beta; interleukin 6 inducer.

OS Homo sapiens.

OS Synthetic.

PN JP03197433-A.

XX 28-AUG-1991.  
 XX PD  
 XX 26-DEC-1989; 89JP-0038998.  
 XX PF  
 XX 26-DEC-1989; 89JP-0038998.  
 XX PR  
 XX (SAKA ) OTSUKA PHARM CO LTD.  
 XX PA  
 XX WPI; 1991-356562/49.  
 XX DR  
 XX IL-6 production inducer - is deriv. of modified amino acid sequence obt'd.  
 XX PT by modification of interleukin I alpha.  
 XX PS Claim 2; Page 2; 17pp; Japanese.  
 XX CC This peptide is a preferred example of an IL-1 beta derivative with IL-6  
 CC inducing activity. Arg at position 98 is deleted. (Updated on 10-MAR-2003  
 CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)  
 CC CC  
 XX SQ Sequence 152 AA;

Query Match 65.1%; Score 54; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10  
 |||||  
 Db 136 TKGQDITDF 145

RESULT 12  
 AAR23670  
 ID AAR23670 standard; protein; 152 AA.  
 XX AC  
 XX AAR23670;  
 XX DT 25-MAR-2003 (revised)  
 DT 30-OCT-1992 (first entry)  
 XX CC  
 XX Interleukin-1 beta delta Gly 50, Gly 51 deletion variant.  
 XX DE  
 XX IL-1; cartilage; metabolism; structural; modifications;  
 KW osteoarticular disease; arthritis.  
 KW Synthetic.  
 XX OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 49..50  
 FT /note= "2 residues deleted from natural sequence"  
 FT  
 XX WO9206114-A.  
 XX PN  
 XX 16-APR-1992.  
 XX PD  
 XX 04-OCT-1991; 91WO-FR000779.  
 XX PF  
 XX 05-OCT-1990; 90FR-00012308.  
 XX PR (RHON ) RHONE-POULENC RORER.  
 XX PA  
 XX Guinet F, Cartwright T, Guitton JD, Terlain B;  
 PI WPI; 1992-150817/18.  
 XX DR N-PSDB; AAQ24073.  
 XX DR Polypeptide(s) derived. from interleukin-1 beta - are useful in treating  
 XX PT osteo-articular disease.  
 XX PS Claim 4; Fig 2D; 27pp; French.  
 XX CC The polypeptide is derived from IL-1 beta and has a deletion mutation in  
 CC the loops between beta sheets (see feature table). Pharmaceutical

CC compans. contg. the IL-1 beta mutant polypeptides are useful in the  
 CC treatment of osteoarticular disease, e.g, arthritis. The deriv. exhibits  
 CC selective inhibition of cartilage metabolism without affecting the immune  
 CC response. See also AAR23668.9. (Updated on 25-MAR-2003 to correct PI  
 CC field.)  
 XX CC  
 XX SQ Sequence 152 AA;

Query Match 65.1%; Score 54; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10  
 |||||  
 Db 136 TKGQDITDF 145

RESULT 13  
 AAP70304  
 ID AAP70304 standard; protein; 153 AA.  
 XX AC  
 XX AAP70304;  
 XX DT 25-MAR-2003 (revised)  
 DT 31-OCT-2002 (revised)  
 DT 05-JUN-1991 (first entry)  
 XX CC  
 XX Sequence of interleukin 1-beta (IL-1-beta).  
 DE  
 XX Cytokine; tumour; therapy; immuno stimulator.  
 KW  
 XX Unidentified.  
 OS  
 XX EP237967-A.  
 PN  
 XX 23-SEP-1987.  
 PD  
 XX 12-MAR-1987; 87EP-00103609.  
 PF  
 XX 14-MAR-1986; 86JP-00057885.  
 PR 20-JUN-1986; 86JP-00145830.  
 PR 09-JUL-1986; 86JP-00161184.  
 PR 27-AUG-1986; 86JP-00200324.  
 PR  
 XX (SAKA ) OTSUKA PHARM CO LTD.  
 PA (HIGU//) HIGUCHI Y.  
 PA  
 XX Nakai S, Kaneta M, Kikumoto Y, Hong YM, Kawai KHS, Azamitsuho M;  
 PI Takegata S, Ishii K;  
 PI WPI; 1987-265364/38.  
 DR  
 XX New interleukin 1-beta analogues - produced by recombinant DNA  
 PT techniques.  
 PT  
 XX Claim 1; Page 47; 49pp; English.  
 XX CC The patent application claims new analogues of IL-1-beta (AAP70304) with  
 CC the following modifications: (a) at least one of Alal, Val3, Arg4, Ser5,  
 CC Cys8, Arg11, His30, Cys71, Lys93, Lys97, Arg98, Phe99, Lys103, Trp120,  
 CC Tyr121 and Ser153 is absent or replaced by another AA; and/or (b) at  
 CC least one AA in the 1-9 sequence is absent; and/or (c) at least one AA in  
 CC the 103-153 sequence is absent; and/or (d) Met, or the 1'-116' sequence  
 CC of (AAP70305) or a C-terminal portion of this sequence is attached to the  
 CC N-terminus of AAP70304. The new analogues are useful for stimulating  
 CC immunity, treating malignant tumours, promoting cytokine prodn., treating  
 CC inflammations, or preventing or curing radiation injuries or  
 CC opportunistic infections. (Updated on 31-OCT-2002 to add missing OS  
 CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-  
 CC 2003 to correct PI field.)  
 XX SQ Sequence 153 AA;

Query Match 65.1%; Score 54; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10  
Db 137 TKGGQDITDF 146

RESULT 14  
AAR04209  
ID AAR04209 standard; protein; 153 AA.  
AC AAR04209;  
XX 25-MAR-2003 (revised)  
DT 12-SEP-1990 (first entry)  
XX  
DE Interleukin - 1 beta sequence.  
XX Human interleukin - 1 beta sequence; vectors; cancer treatment;  
KW signal sequence; human growth hormone.  
XX Synthetic.  
OS  
XX  
FN FR2636231-A.  
XX  
PD 16-MAR-1990.  
PF 09-SEP-1988; 88FR-00011833.  
XX  
PR 09-SEP-1988; 88FR-00011833.  
XX  
PA (SNFI) SANOFI SA.  
XX  
PI Pecceu F, Lupker J;  
XX  
DR WPI; 1990-134114/18.  
DR N-PSDB; AAQ04074.  
XX  
PT Eukaryotic cell producing interleukin 1-beta - in glycosylated mature  
form, and new vectors contg. coding and signal sequences.  
XX  
PS Disclosure; Page ?; -pp; French.  
XX  
CC Eukaryotic cells containing expression vectors containing the sequence  
encoding mature IL-1 beta preceded by DNA sequence coding for the signal  
peptide of a natural precursor of human growth hormone, produce N-  
glycosylated mature IL-1 beta. The product is useful in medicine, eg for  
treating cancer and infectious or parasitic diseases. (Updated on 25-MAR-  
2003 to correct PF field.)  
XX  
SQ Sequence 153 AA;

Query Match 65.1%; Score 54; DB 2; Length 153;  
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10  
Db 137 TKGGQDITDF 146

RESULT 15  
AAR05386  
ID AAR05386 standard; protein; 153 AA.  
XX  
AC AAR05386;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAR-2003 (revised)  
DT 15-OCT-1990 (first entry)  
XX

DE polypeptide with physiological activity of interleukin-I-Beta (IL-1-beta).  
XX Interleukin; IL-1-Beta.  
XX Unidentified.  
OS  
XX Key Location/Qualifiers  
FH Misc-difference 35 /label= Asp Asn or Ser  
FT Misc-difference 37 /label= Glu Gln or Ser  
FT Misc-difference 152 /label= Ser or Arg  
FT  
XX JP02119793-A.  
PN  
XX 07-MAY-1990.  
PD  
XX 28-OCT-1988; 88JP-00272019.  
PF  
XX 28-OCT-1988; 88JP-00272019.  
PR  
XX (YAMA) YAMANOUCHI PHARM CO LTD.  
PA  
XX WPI; 1990-182391/24.  
DR N-PSDB; AAQ04737.  
XX  
PT Polypeptide useful in pharmaceuticals - having physiological action  
similar to that of interleukin-I-beta.  
XX  
PS Claim 1; Page 839; 22pp; Japanese.  
XX  
CC Polypeptide has physiological activities similar but improved to IL-1-  
beta. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-  
MAR-2003 to correct PA field.)  
XX  
SQ Sequence 153 AA;

Query Match 65.1%; Score 54; DB 2; Length 153;  
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10  
Db 137 TKGGQDITDF 146

Search completed: January 5, 2006, 21:43:00  
Job time : 188 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 5, 2006, 21:39:51 ; Search time 165 Seconds  
(without alignments)  
40.517 Million cell updates/sec

Title: US-09-894-550-3  
Perfect score: 83  
Sequence: 1 TKGGQDITDFQILENQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	16	3	US-09-894-550-3
2	54	65.1	70	4	US-10-716-029-200
3	54	65.1	133	5	US-10-637-313-80
4	54	65.1	151	4	US-10-003-671A-23
5	54	65.1	153	3	US-09-775-046-6
6	54	65.1	153	3	US-09-894-550-4
7	54	65.1	153	4	US-10-095-407-15
8	54	65.1	153	4	US-10-139-833-8
9	54	65.1	153	4	US-10-139-947-6
10	54	65.1	153	4	US-10-469-165-4
11	54	65.1	153	4	US-10-735-354-6
12	54	65.1	153	5	US-10-872-198-112
13	54	65.1	153	6	US-11-021-951-112
14	54	65.1	154	4	US-10-695-195-9
15	54	65.1	154	4	US-10-694-978-9
16	54	65.1	219	5	US-10-637-313-78
17	54	65.1	219	5	US-10-637-313-84
18	54	65.1	219	5	US-10-637-313-86
19	54	65.1	219	5	US-10-637-313-88
20	54	65.1	219	5	US-10-637-313-90
21	54	65.1	219	5	US-10-637-313-92
22	54	65.1	269	3	US-09-840-707A-2
23	54	65.1	269	3	US-09-770-528-10
24	54	65.1	269	4	US-10-139-833-7
25	54	65.1	269	4	US-10-011-931-2
26	54	65.1	269	4	US-10-038-557A-2
27	54	65.1	269	4	US-10-167-127-4

28	54	65.1	269	4	US-10-440-464-53	Sequence 53, Appl
29	54	65.1	269	4	US-10-447-315-13	Sequence 13, Appl
30	54	65.1	269	5	US-10-637-313-82	Sequence 82, Appl
31	54	65.1	269	5	US-10-985-299-2	Sequence 2, Appl
32	54	65.1	269	5	US-10-491-997-84	Sequence 84, Appl
33	53	63.9	66	4	US-10-716-029-187	Sequence 187, Appl
34	53	63.9	145	3	US-09-775-046-5	Sequence 5, Appl
35	53	63.9	159	4	US-10-695-195-5	Sequence 5, Appl
36	53	63.9	159	4	US-10-694-978-5	Sequence 2, Appl
37	53	63.9	159	4	US-10-469-165-2	Sequence 25, Appl
38	53	63.9	271	3	US-09-854-280-25	Sequence 1, Appl
39	53	63.9	271	3	US-09-840-707A-1	Sequence 25, Appl
40	53	63.9	271	3	US-09-854-208-25	Sequence 7, Appl
41	53	63.9	271	3	US-09-919-172-7	Sequence 6, Appl
42	53	63.9	271	3	US-09-974-298-6	Sequence 11, Appl
43	53	63.9	271	4	US-09-770-528-11	Sequence 1, Appl
44	53	63.9	271	4	US-10-011-931-1	Sequence 1, Appl
45	53	63.9	271	4	US-10-038-557A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-894-550-3  
; Sequence 3, Application US/09894550  
; Publication No. US20030040083A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Collinson, Albert  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Avgerinos, George  
; APPLICANT: Dixon, Richard  
; APPLICANT: Kaymakalan, Zehra  
; TITLE OF INVENTION: DUAL SPECIFICITY ANTIBODIES AND METHODS OF MAKING AND USING  
; FILE REFERENCE: BBC-083A US  
; CURRENT APPLICATION NUMBER: US/09/894,550  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 60/215,379  
; PRIOR FILING DATE: 2000-06-29  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hybrid peptide  
US-09-894-550-3

Query Match 100.0%; Score 83; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDFQILENQ 16  
|||||  
DB 1 TKGGQDITDFQILENQ 16

RESULT 2  
US-10-716-029-200  
; Sequence 200, Application US/10716029  
; Publication No. US20040171038A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicklin, Martin  
; APPLICANT: Duff, Gordon  
; APPLICANT: Kornman, Kenneth  
; APPLICANT: Kolpin, Maryam R  
; APPLICANT: Hsieh, Chung-Ming  
; APPLICANT: Govindaraju, Raju  
; APPLICANT: Aziz, Nazneen  
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms  
; TITLE OF INVENTION: and Haplotypes

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; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 200
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-029-200

Query Match 65.1%; Score 54; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 54 TKGQDITDF 63

RESULT 3
US-10-637-313-80
; Sequence 80, Application US/10637313
; Publication No. US2004022979A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khrantsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 80
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-637-313-80

Query Match 65.1%; Score 54; DB 5; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 115 TKGQDITDF 124

RESULT 4
US-10-003-671A-23
; Sequence 23, Application US/10003671A
; Publication No. US20020156009A1
; GENERAL INFORMATION:
; APPLICANT: MIZE, ET AL
; TITLE OF INVENTION: NOVEL INTERLEUKIN-1 HY2 MATERIALS AND METHODS
; FILE REFERENCE: 28110/36858A
; CURRENT APPLICATION NUMBER: US/10/003,671A
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/245,346
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-671A-23

Query Match 65.1%; Score 54; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 135 TKGQDITDF 144

RESULT 5
US-09-775-046-6
; Sequence 6, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-6

Query Match 65.1%; Score 54; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146

RESULT 6
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US-09-894-550-4
; Sequence 4, Application US/09894550
; Publication No. US20030040083A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Collinson, Albert
; APPLICANT: Ghayur, Tariq
; APPLICANT: Agerinos, George
; APPLICANT: Dixon, Richard
; APPLICANT: Kaymakalan, Zehra
; TITLE OF INVENTION: DUAL SPECIFICITY ANTIBODIES AND METHODS OF MAKING AND USING
; FILE REFERENCE: BPC-083A US
; CURRENT APPLICATION NUMBER: US/09/894,550
; CURRENT FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hybrid peptide
US-09-894-550-4

Query Match      65.1%; Score 54; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146

RESULT 7
US-10-095-407-15
; Sequence 15, Application US/10095407
; Publication No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-095-407-15

Query Match      65.1%; Score 54; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146

RESULT 8
US-10-139-833-8
; Sequence 8, Application US/10139833
; Publication No. US20030004106A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
```

```
; APPLICANT: Giles, Jennifer
; APPLICANT: Mu, Sharon X.
; APPLICANT: Xia, Min
; APPLICANT: Bass, Michael B.
; APPLICANT: Craveiro, Roger
; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-1213-E
; CURRENT APPLICATION NUMBER: US/10/139,833
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/170,191
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/188,053
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/194,521
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 60/195,910
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 09/724,583
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-833-8

Query Match      65.1%; Score 54; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146

RESULT 9
US-10-139-947-6
; Sequence 6, Application US/10139947
; Publication No. US20030166069A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Jing, Shudian
; APPLICANT: Luethy, Roland
; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-1214-E
; CURRENT APPLICATION NUMBER: US/10/139,947
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/170,052
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 09/723,676
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-947-6

Query Match      65.1%; Score 54; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146

RESULT 10
US-10-469-165-4
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; Sequence 4, Application US/10469165
; Publication No. US20040103447A1
; GENERAL INFORMATION:
; APPLICANT: NAWA, Hiroyuki
; TITLE OF INVENTION: SCHIZOPHRENIA-LIKE MENTAL DISEASE MODEL ANIMAL, METHOD OF
; TITLE OF INVENTION: CONSTRUCTING THE SAME AND USE THEREOF
; FILE REFERENCE: 224167
; CURRENT APPLICATION NUMBER: US/10/469,165
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/JP02/01734
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: JP 2001-52546
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-165-4
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Query Match 65.1%; Score 54; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146
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## RESULT 11

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US-10-735-354-6
; Sequence 6, Application US/10735354
; Publication No. US20040208872A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Jing, Shuqian
; APPLICANT: Luethy, Roland
; TITLE OF INVENTION: Nucleic Acids Encoding Interleukin-1 Receptor Antagonist-
; FILE REFERENCE: 00-1214-P
; CURRENT APPLICATION NUMBER: US/10/735,354
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/723,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/170,052
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-354-6
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```
Query Match 65.1%; Score 54; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146
|||||
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## RESULT 12

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US-10-872-198-112
; Sequence 112, Application US/10872198
; Publication No. US2005002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
```

```
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-112
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Query Match 65.1%; Score 54; DB 5; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TKGQDITDF 10
Db 137 TKGQDITDF 146
|||||
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## RESULT 13

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US-11-021-951-112
; Sequence 112, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOETSMEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-112
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Query Match 65.1%; Score 54; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10  
DB 137 TKGGQDITDF 146

## RESULT 14

US-10-695-195-9  
; Sequence 9, Application US/10695195  
; Publication No. US20040068099A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/695,195  
FILING DATE: 27-Oct-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,412  
FILING DATE: 17-Sep-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DXO904K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-9196  
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-695-195-9

Query Match 65.1%; Score 54; DB 4; Length 154;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10  
DB 138 TKGGQDITDF 147

## RESULT 15

US-10-694-978-9  
; Sequence 9, Application US/10694978  
; Publication No. US20040087766A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: DNAX Research Institute  
; STREET: 901 California Avenue

CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/694,978  
FILING DATE: 27-Oct-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,412  
FILING DATE: 17-Sep-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DXO904K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-9196  
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-694-978-9

Query Match 65.1%; Score 54; DB 4; Length 154;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10  
DB 138 TKGGQDITDF 147

Search completed: January 5, 2006, 21:51:25  
Job time : 166 secs

***This Page Blank (user)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 5, 2006, 21:39:36 ; Search time 46 Seconds  
(without alignments)  
28.757 Million cell updates/sec

Title: US-09-894-550-3

Perfect score: 83

Sequence: 1 TKGGQDITDQILENQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents: AA:\*

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2: /cgm2\_6/ptodata/1/iaa/6 COMB.pep:\*

3: /cgm2\_6/ptodata/1/iaa/H COMB.pep:\*

4: /cgm2\_6/ptodata/1/iaa/PTUS COMB.pep:\*

5: /cgm2\_6/ptodata/1/iaa/RE COMB.pep:\*

6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	56	67.5	271	2	US-09-085-305-15
3	54	65.1	18	6	5217714-5
4	54	65.1	32	1	US-08-127-351-11
5	54	65.1	32	1	US-08-480-367B-11
6	54	65.1	32	1	US-08-487-221A-11
7	54	65.1	32	1	US-08-480-370-11
8	54	65.1	147	6	US-08-354-456A-8
9	54	65.1	147	6	5217714-2
10	54	65.1	148	6	5217714-3
11	54	65.1	152	6	5217714-6
12	54	65.1	153	1	US-08-100-744-2
13	54	65.1	153	1	US-08-284-784-2
14	54	65.1	153	1	US-08-139-862-3
15	54	65.1	153	1	US-08-599-895-13
16	54	65.1	153	1	US-08-854-811-2
17	54	65.1	153	2	US-09-211-290-13
18	54	65.1	153	2	US-09-030-613-13
19	54	65.1	153	2	US-09-322-676-13
20	54	65.1	153	2	US-09-128-155-15
21	54	65.1	153	2	US-09-466-036A-13
22	54	65.1	153	2	US-09-451-905-13
23	54	65.1	153	2	US-09-775-046-6
24	54	65.1	153	6	5217714-1
25	54	65.1	153	6	5217714-4
26	54	65.1	154	2	US-09-398-412B-9
27	54	65.1	269	1	US-08-203-716-3

28 54 65.1 269 1 US-08-440-179-3 Sequence 3, Appli  
29 54 65.1 269 1 US-08-432-693-11 Sequence 11, Appl  
30 54 65.1 269 1 US-08-599-895-11 Sequence 11, Appl  
31 54 65.1 269 1 US-08-483-806-2 Sequence 2, Appli  
32 54 65.1 269 2 US-09-211-290-11 Sequence 11, Appl  
33 54 65.1 269 2 US-09-030-613-11 Sequence 11, Appl  
34 54 65.1 269 2 US-09-322-676-11 Sequence 11, Appl  
35 54 65.1 269 2 US-09-039-657-3 Sequence 3, Appli  
36 54 65.1 269 2 US-08-748-547-4 Sequence 4, Appli  
37 54 65.1 269 2 US-09-466-036A-11 Sequence 11, Appl  
38 54 65.1 269 2 US-09-451-905-11 Sequence 11, Appl  
39 54 65.1 269 2 US-09-949-016-5960 Sequence 5960, Ap  
40 54 65.1 269 4 PCT-US91-02339-1 Sequence 1, Appli  
41 54 65.1 298 2 US-09-949-016-11362 Sequence 11362, A  
42 53 63.9 145 2 US-09-030-613-9 Sequence 9, Appli  
43 53 63.9 145 2 US-09-451-905-9 Sequence 9, Appli  
44 53 63.9 145 2 US-09-775-046-5 Sequence 5, Appli  
45 53 63.9 153 1 US-08-100-744-3 Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-085-305-12  
; Sequence 12, Application US/09085305  
; Patent No. 6191269

GENERAL INFORMATION:  
APPLICANT: Pollock, Allan

APPLICANT: Lovett, David H.  
APPLICANT: Turck, Johanna

TITLE OF INVENTION: Selective Induction of Apoptosis in  
Malignant Cancer Cells by Delivery of N-Terminal  
Interleukin-1-Alpha Pro-Piece Polypeptide

TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Ave, Suite 200

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/085,305

FILING DATE: 29-MAY-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Francis, Carol L

REGISTRATION NUMBER: 36,513

REFERENCE/DOCKET NUMBER: 6510/102US1

TELEPHONE: 650-327-3400

TELEFAX: 650-327-3231

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 271 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6191269e

US-09-085-305-12

Query Match 67.5%; Score 56; DB 2; Length 271;  
Best Local Similarity 80.0%; Pred. No. 0.089;



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1 GENERAL INFORMATION:
2 APPLICANT: BELINKA Jr, BENJAMIN A.
3 APPLICANT: COUGHLIN, DANIEL J.
4 APPLICANT: ALVAREZ, VERNON L.
5 APPLICANT: WOOD, RICHARD
6 TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
7 TITLE OF INVENTION: CONSTRUCTS
8 NUMBER OF SEQUENCES: 56
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
11 STREET: 99 Canal Center Plaza, Suite 300
12 CITY: Alexandria
13 STATE: Virginia
14 COUNTRY: U.S.A.
15 ZIP: 22314
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatenIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/480,367B
23 FILING DATE: 07-06-95
24 CLASSIFICATION: 424
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Villacorta, Gilberto M.
27 REGISTRATION NUMBER: 34,038
28 REFERENCE/DOCKET NUMBER: 2654-002A
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (703) 684-1111
31 TELEFAX: (703) 684-1124
32 TELEX:
33 INFORMATION FOR SEQ ID NO: 11:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 32 amino acids
36 TYPE: amino acid
37 TOPOLOGY: unknown
38 MOLECULE TYPE: peptide
39
40 US-08-480-367B-11

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Query Match	65.1%	Score 54;	DB 1;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 0.018;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels	
QY	1	TKGGQDITDF	10	
Dh	21	TKGGQDITDF	30	

RESULT 6  
US-08-487-221A-11  
; Sequence 11, Application US/08487221A  
; Patent No. 5593656  
; GENERAL INFORMATION:  
; APPLICANT: BELINKA Jr, BENJAMIN A.  
; APPLICANT: COUGHLIN, DANIEL J.  
; APPLICANT: ALVAREZ, VERNON L.  
; APPLICANT: WOOD, RICHARD  
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
; TITLE OF INVENTION: CONSTRUCTS  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
; ADDRESSEE: NEUSTADT, P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; City: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,221A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248955 OPAT UR  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-487-221A-11

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Query Match      65.1%; Score 54; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	TKGGQDITDF	10
nb	21	TKGGQDITDF	30

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RESULT 7
US-08-480-370-11
; Sequence 11, Application US/08480370
; Patent No. 5609847
;
; GENERAL INFORMATION:
; APPLICANT: BELINKA Jr., BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
;
; NUMBER OF SEQUENCES: 56
;
; CORRESPONDENCE ADDRESS:
; ADDRESSES: OBOLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSES: NEUSTADT,
; ADDRESSES: P.C.
; CITY: Arlington
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; STATE: Virginia
; COUNTRY: U.S.A.

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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,370  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220

```
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-370-11

Query Match 65.1%; Score 54; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
Db 21 TKGGQDITDF 30

RESULT 8
US-08-354-456A-8
; Sequence 8, Application US/08354456A
; Patent No. 5567611
; GENERAL INFORMATION:
; APPLICANT: Ralph, Peter
; APPLICANT: Martin, George
; APPLICANT: Platek, Michael
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,456A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,338
; FILING DATE: 21-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 750.003/32387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-354-456A-8

Query Match 65.1%; Score 54; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
Db 1 TKGGQDITDF 10
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Db 134 TKGGQDITDF 143

RESULT 9
5217714-2
; Patent No. 5217714
; APPLICANT: IMURA, HIROO; FUKATA, JUNICHI; HIRAI, YOSHIKATSU
; TITLE OF INVENTION: METHOD FOR STIMULATING THE SECRETION
; OF ACTH BY ADMINISTRATION OF IL-1B ANALOGUES
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409,193
; FILING DATE: 19-SEP-1989
; SEQ ID NO: 2:
; LENGTH: 147
5217714-2

Query Match 65.1%; Score 54; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
Db 131 TKGGQDITDF 140

RESULT 10
5217714-3
; Patent No. 5217714
; APPLICANT: IMURA, HIROO; FUKATA, JUNICHI; HIRAI, YOSHIKATSU
; TITLE OF INVENTION: METHOD FOR STIMULATING THE SECRETION
; OF ACTH BY ADMINISTRATION OF IL-1B ANALOGUES
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409,193
; FILING DATE: 19-SEP-1989
; SEQ ID NO: 3:
; LENGTH: 148
5217714-3

Query Match 65.1%; Score 54; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
Db 137 TKGGQDITDF 146

RESULT 11
5217714-6
; Patent No. 5217714
; APPLICANT: IMURA, HIROO; FUKATA, JUNICHI; HIRAI, YOSHIKATSU
; TITLE OF INVENTION: METHOD FOR STIMULATING THE SECRETION
; OF ACTH BY ADMINISTRATION OF IL-1B ANALOGUES
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409,193
; FILING DATE: 19-SEP-1989
; SEQ ID NO: 6:
; LENGTH: 152
5217714-6

Query Match 65.1%; Score 54; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10
Db 136 TKGGQDITDF 145

RESULT 12
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US-08-100-744-2  
 ; Sequence 2, Application US/08100744  
 ; Patent No. 5563046  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MASCARENHAS, DESMOND  
 ; APPLICANT: ZHANG, SUNNY  
 ; APPLICANT: OLSON, PAMELA  
 ; APPLICANT: OLSEN, DAVID  
 ; APPLICANT: CARRILLO, PEDRO A.  
 ; TITLE OF INVENTION: POLYPEPTIDE FUSIONS TO  
 ; INTERLEUKIN-1-LIKE POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/100,744  
 ; FILING DATE: 02-AUG-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: LUTHER, BARBARA J.  
 ; REGISTRATION NUMBER: 33,954  
 ; REFERENCE/DOCKET NUMBER: 22095-20275.00  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 153 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-100-744-2

Query Match 65.1%; Score 54; DB 1; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10  
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 Db 137 TKGGQDITDF 146

RESULT 13  
 US-08-284-784-2  
 ; Sequence 2, Application US/08284784  
 ; Patent No. 5629172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MASCARENHAS, DESMOND  
 ; APPLICANT: ZHANG, YANG  
 ; APPLICANT: OLSON, PAMELA S.  
 ; APPLICANT: OLSEN, DAVID R.  
 ; APPLICANT: CARRILLO, PEDRO A.  
 ; TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES  
 ; TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/08/284,784  
 APPLICATION NUMBER: US/08/284,784  
 FILING DATE: 02-AUG-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARK, FREDDIE K.  
 REGISTRATION NUMBER: 35,636  
 REFERENCE/DOCKET NUMBER: 22095-20275.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 153 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 ; US-08-284-784-2

Query Match 65.1%; Score 54; DB 1; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKGGQDITDF 10  
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 Db 137 TKGGQDITDF 146

RESULT 14  
 US-08-139-862-3  
 ; Sequence 3, Application US/08139862  
 ; Patent No. 5723117  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAI, Satoru  
 ; APPLICANT: AKAMATSU, Seiji  
 ; APPLICANT: MASUI, Yoshihiro  
 ; APPLICANT: NISHIDA, Tsutomu  
 ; APPLICANT: KAMOGASHIRA, Takashi  
 ; APPLICANT: HIRAI, Yoshikatu  
 ; TITLE OF INVENTION: AGENT FOR PREVENTING AND TREATING  
 ; HEPATITIS  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 ; STREET: 2100 Pennsylvania Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/139,862  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/839,770  
 ; FILING DATE: 09-APR-1992  
 ; CLASSIFICATION: 424  
 ; APPLICATION NUMBER: JP 212941/1990  
 ; FILING DATE: 10-AUG-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/JP91/01067  
 ; FILING DATE: 09-AUG-1991

Search completed: January 5, 2006, 21:48:34  
Job time : 46 secs

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon  
REGISTRATION NUMBER: 30,764  
REFERENCE/DOCKET NUMBER: Q-28983  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: Peptide  
FRAGMENT TYPE: N-terminal  
US-08-139-862-3

Query Match 65.1%; Score 54; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10  
Db 137 TKGGQDITDF 146

RESULT 15

US-08-599-895-13  
Sequence 13, Application US/08599895  
Patent No. 5891855  
GENERAL INFORMATION:  
APPLICANT: Flokiewicz, Robert Z.  
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,895  
FILING DATE: 31-JAN-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5891855tenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.416  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-599-895-13

Query Match 65.1%; Score 54; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKGGQDITDF 10  
Db 137 TKGGQDITDF 146